

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:09:53 ; Search time 13.35 Seconds
(without alignments)
240.606 Million cell updates/sec

Title: US-09-016-869A-2

Perfect score: 156

Sequence: 1 MDPAGSMPSADWLATAA.....TRGSNHARIDAAGPSDIPD 156

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 197339 seqs, 20590346 residues

size : 0
Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2.6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	100.0	156	2	US-08-627-610-2
2	156	100.0	156	2	US-08-306-511A-2
3	156	100.0	156	2	US-08-893-274-2
4	156	100.0	156	3	US-08-581-918A-2
5	156	100.0	156	4	US-08-346-147B-2
6	156	100.0	156	4	US-08-822-936-2
7	156	100.0	156	5	PCT-US95-04636-2
8	153	98.1	391	1	US-08-589-981-2
9	148	94.9	148	1	US-08-154-915-4
10	148	94.9	148	3	US-08-384-106A-16
11	148	94.9	148	3	US-08-384-106A-24
12	148	94.9	148	5	PCT-US93-09945-4
13	141	77.6	156	1	US-08-474-177-2
14	121	77.6	156	1	US-08-487-033-2
15	121	77.6	156	1	US-08-480-810-2
16	121	77.6	156	2	US-08-508-735-2
17	121	77.6	156	2	US-08-848-251-2
18	121	77.6	156	2	US-08-486-047-2
19	121	77.6	156	3	US-09-120-130-2
20	121	77.6	156	3	US-09-115-252-2
21	121	77.6	156	3	US-08-986-515-2
22	121	77.6	156	4	US-09-120-128-2
23	121	77.6	156	4	US-09-120-129-2
24	121	77.6	156	4	US-09-201-139-2
25	121	77.6	156	4	US-09-120-131-2
26	121	77.6	156	4	US-08-910-722-2
27	105	67.3	105	1	US-08-474-177-14

28	105	67.3	105	1	US-08-487-033-14	Sequence 14, Appl
29	105	67.3	105	1	US-08-480-810-14	Sequence 14, Appl
30	105	67.3	105	2	US-08-508-735-14	Sequence 14, Appl
31	105	67.3	105	2	US-08-848-251-14	Sequence 14, Appl
32	105	67.3	105	2	US-08-486-047-14	Sequence 14, Appl
33	105	67.3	105	3	US-09-120-130-14	Sequence 14, Appl
34	105	67.3	105	3	US-09-115-252-14	Sequence 14, Appl
35	105	67.3	105	3	US-08-986-515-14	Sequence 14, Appl
36	105	67.3	105	4	US-09-120-128-14	Sequence 14, Appl
37	105	67.3	105	4	US-09-120-129-14	Sequence 14, Appl
38	105	67.3	105	4	US-09-201-139-14	Sequence 14, Appl
39	105	67.3	105	4	US-09-120-131-14	Sequence 14, Appl
40	95	60.9	157	5	PCT-US96-05252-5	Sequence 5, Appl
41	89	57.1	89	3	US-08-581-918A-37	Sequence 37, Appl
42	89	57.1	89	4	US-08-346-147B-37	Sequence 38, Appl
43	72	46.2	88	3	US-08-581-918A-38	Sequence 38, Appl
44	72	46.2	88	4	US-08-346-147B-38	Sequence 38, Appl
45	72	46.2	136	5	PCT-US96-05252-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-627-610-2
; Sequence 2, Application US/08627610
; Patent No. 591997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: Depinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; TITLE OF INVENTION: Regulation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-627-610-2

Query Match 100.0%; Score 156; DB 2; Length 156;
Best Local Similarity 100.0%; Pred No. 8.7e-138; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 0;
QY 1 MDPAGSMPSADWLATAAARGVEEVRRALLEVALPNAPNSYGRRPQVNMMSARVA 60
Db 1 MDPAGSMPSADWLATAAARGVEEVRRALLEVALPNAPNSYGRRPQVNMMSARVA 60

QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAAE 120
|||||
Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAAE 120
|||||

QY 121 LGRDVARYLRAAAGTRGSNHARIDAAGPSDIPD 156
|||||
Db 121 LGRDVARYLRAAAGTRGSNHARIDAAGPSDIPD 156
|||||

RESULT 2

US-08-306-511A-2

; Sequence 2, Application US/08306511A

; Patent No. 5962316

; GENERAL INFORMATION:

; APPLICANT: Beach, David H.

; APPLICANT: Demetrick, Douglas J.

; APPLICANT: Serrano, Manuel

; APPLICANT: Hannon, Gregory J.

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

; TITLE OF INVENTION: Related Thereto

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/306.511A

; FILING DATE: 14-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: CSI-001CP2

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-306-511A-2

Query Match 100.0%; Score 156; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 8.7e-138;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAAGSSMEPSADWLATAAARGVEEVRALLEVALPNAFNSYGRPRPIQVMMGSRVA 60
|||||

Db 1 MDPAAAGSSMEPSADWLATAAARGVEEVRALLEVALPNAFNSYGRPRPIQVMMGSRVA 60
|||||

QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAAE 120
|||||

Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAAE 120
|||||

QY 121 LGRDVARYLRAAAGTRGSNHARIDAAGPSDIPD 156
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Db 121 LGRDVARYLRAAAGTRGSNHARIDAAGPSDIPD 156
|||||

RESULT 3

US-08-893-274-2

; Sequence 2, Application US/08893274

; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/893.274

; FILING DATE: 15-JULY-1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/306,511

; FILING DATE: 14-SEPTEMBER-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/248,812

; FILING DATE: 25-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/227,371

; FILING DATE: 14-APRIL-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/154,915

; FILING DATE: 18-NOVEMBER-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/991,997

; FILING DATE: 17-DECEMBER-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/963,308

; FILING DATE: 16-OCTOBER-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-071.09

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 832-1000

; TELEFAX: (617) 832-7000

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-893-274-2

Query Match 100.0%; Score 156; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 8.7e-138;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAAGSSMEPSADWLATAAARGVEEVRALLEVALPNAFNSYGRPRPIQVMMGSRVA 60
|||||

Db 1 MDPAAAGSSMEPSADWLATAAARGVEEVRALLEVALPNAFNSYGRPRPIQVMMGSRVA 60
|||||

QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAAE 120
|||||

Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAAE 120
|||||

QY 121 LGRDVARYLRAAAGTRGSNHARIDAAGPSDIPD 156
|||||

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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:10:53 ; Search time 14.49 Seconds
(without alignments)
820.099 Million cell updates/sec

Title: US-09-016-869A-2
Perfect score: 156
Sequence: 1 MDPAGSSMEPSADWLATRA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

size : 0
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	121	77.6	JF0141	cyclin dependent k
2	72	46.2	B55479	CDK4 inhibitor p14
3	48	30.8	I78845	p15INK4b - mouse
4	34	21.8	I52720	gene p15INK4B prot
5	19	12.2	I58352	p16INK4a - mouse
6	8	5.1	G69303	iron (III) ABC tra
7	8	5.1	T43647	hypothetical prote
8	5.1	1691	A44212	genome polyprotein
9	8	5.1	MBWHRH	hypothetical prote
10	7	4.5	I422	hypothetical prote
11	7	4.5	B72683	ORF3 protein - Orf
12	7	4.5	I5792	cyclin-dependent k
13	7	4.5	E34768	CDK4/Cdk6 inhibito
14	7	4.5	A57378	cyclin-dependent k
15	7	4.5	B57379	probable nicotinam
16	7	4.5	T36141	alcohol dehydrogen
17	7	4.5	B3724	alcohol dehydrogen
18	7	4.5	C23724	alcohol dehydrogen
19	7	4.5	D33724	ABC transporter, A
20	7	4.5	A75304	probable enoyl-CoA
21	7	4.5	H83425	purine nucleoside
22	7	4.5	D69980	transcription regu
23	7	4.5	F82977	alcohol dehydrogen
24	7	4.5	DEFFRL	alcohol dehydrogen
25	7	4.5	A40553	alcohol dehydrogen
26	7	4.5	S15711	alcohol dehydrogen
27	7	4.5	S15712	alcohol dehydrogen
28	7	4.5	S06001	alcohol dehydrogen
29	7	4.5	B24268	alcohol dehydrogen

30	7	4.5	254	1	A24268	alcohol dehydrogen
31	7	4.5	254	1	S01901	alcohol dehydrogen
32	7	4.5	254	1	E23724	alcohol dehydrogen
33	7	4.5	254	2	A23724	alcohol dehydrogen
34	7	4.5	254	2	D72464	hypothetical prote
35	7	4.5	273	2	T34740	hypothetical prote
36	7	4.5	283	2	E84258	hypothetical prote
37	7	4.5	314	2	D70313	riboflavin kinase
38	7	4.5	318	1	F70536	3',5'-cyclic-nucle
39	7	4.5	331	2	D86413	probable cysteine
40	7	4.5	334	2	A82751	ABC transporter AT
41	7	4.5	345	2	B84752	probable cysteine
42	7	4.5	346	2	C86413	probable cysteine
43	7	4.5	348	2	T18230	alcohol dehydrogen
44	7	4.5	348	2	T35450	ABC transporter AT
45	7	4.5	353	2	D75553	branched-chain ami

ALIGNMENTS

RESULT 1

JE0141
cyclin dependent kinase inhibitor - human
N:Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor
C:Species: Homo sapiens (man)
C>Date: 02-Jun-1998 #sequence revision 10-Jul-1998 #text_change 19-May-2000
C:Accession: JE0141; I59268; S39359; I59585; JC5679
R:Huang, C.G.; Deng, W.; Fu, J.L.
Chin. J. Biotechnol. 13, 105-107, 1997
A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.
A:Reference number: JE0141
A:Accession: JE0141
A:Molecule type: mRNA
A:Residues: 1-156 <HUA>
R:Experimental source: Hella cell
R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett,
Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994
A:Title: Mutations and altered expression of p16INK4 in human cancer.
A:Reference number: I59268; MUID:95062202
A:Accession: I59268
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-152 <OKA>
A:Cross-references: GB:I27211; NID:g558656; PIDN:AAA92554.1; PID:g558657
A:Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AAA925
R:Serrano, M.; Hannon, G.J.; Beach, D.
Nature 366, 704-707, 1993
A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of
A:Reference number: S39359; MUID:94081956
A:Accession: S39359
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 9-34, 'V', 36-156 <SER>
A:Note: this sequence is corrected in reference I59268
R:Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.;
Science 264, 436-440, 1994
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.
A:Reference number: I59585; MUID:94204645
A:Accession: I59585
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 51-152 <KAM>
A:Cross-references: GB:S69804; NID:g546272; PIDN:AAD14048.1; PID:g4261748
C:Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 ki
C:Genetics:
A:Gene: GDB:CDKN2A; CDK4.I; MLM; P16; INK4; MTS1; CMM2; CDKN2
A:Cross-references: GDB:335362; OMIM:600160
A:Map position: 9p21-9p21
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:14:44 ; Search time 9.37 seconds
(without alignments)
570.315 Million cell updates/sec

Title: US-09-016-869A-2
Perfect score: 156
Sequence: 1 MDPAGSSMEPSADWLATRA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	77.6	156	1	CDN2_HUMAN
2	72	46.2	138	1	CDN5_HUMAN
3	48	30.8	130	1	CDN5_MOUSE
4	36	23.1	130	1	CDN5_RAT
5	19	12.2	167	1	CDN2_MOUSE
6	14	9.0	171	1	CDN2_MONDO
7	8	5.1	1693	1	POLN_HEVME
8	8	5.1	1693	1	POLN_HEVBU
9	8	5.1	1693	1	POLN_HEVNY
10	8	5.1	1693	1	POLN_HEVPA
11	7	4.5	166	1	CDN7_HUMAN
12	7	4.5	166	1	CDN7_MOUSE
13	7	4.5	218	1	GPH_RHOSH
14	7	4.5	231	1	MTN_BACSU
15	7	4.5	253	1	ADH1_DROHY
16	7	4.5	253	1	ADH1_DROMU
17	7	4.5	253	1	ADH1_DROMU
18	7	4.5	253	1	ADH1_DRONA
19	7	4.5	253	1	ADH2_DROAR
20	7	4.5	253	1	ADH2_DROBU
21	7	4.5	253	1	ADH2_DROHY
22	7	4.5	253	1	ADH2_DROMO
23	7	4.5	253	1	ADH2_DROMU
24	7	4.5	253	1	ADH2_DROMY
25	7	4.5	253	1	ADH2_DROWH
26	7	4.5	253	1	ADH_DROAD
27	7	4.5	253	1	ADH_DROAF
28	7	4.5	253	1	ADH_DRODI
29	7	4.5	253	1	ADH_DROGR
30	7	4.5	253	1	ADH_DROHA
31	7	4.5	253	1	ADH_DROHE
32	7	4.5	253	1	ADH_DROMM
33	7	4.5	253	1	ADH_DRONI

RESULT	1	253	4.5	7	4.5	253	1	ADH_DROPI	P23361 drosophila
CDN2_HUMAN	AC	P42771	Q15191	STANDARD	PRT	156 AA			
DT	01-NOV-1995	(Rel. 32, Created)							
DT	15-JUL-1998	(Rel. 36, Last sequence update)							
DT	01-OCT-2000	(Rel. 40, Last annotation update)							
DE	CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)								
DE	(MULTIPLE TUMOR SUPPRESSOR 1) (MTS1).								
GN	CDKN2A OR CDKN2								
OS	Homo sapiens (Human)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
CB	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=94081956; PubMed=8259215;								
RA	Serrano M., Hannon G.J., Beach D.								
RT	"A new regulatory motif in cell-cycle control causing specific								
RT	inhibition of cyclin D/CDK4."								
RL	Nature 366:704-707(1993).								
RN	[2]								
RX	SEQUENCE OF 51-152 FROM N.A.								
RX	MEDLINE=94204645; PubMed=8153634;								
RA	Kamb A., Guis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,								
RA	Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,								
RA	Skolnick M.H.;								
RT	"A cell cycle regulator potentially involved in genesis of many tumor								
RT	types."								
RL	Science 264:436-440(1994).								
RN	[3]								
RX	SEQUENCE OF 1-20 FROM N.A.								
RX	MEDLINE=96182088; PubMed=8622687;								
RA	Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;								
RT	"Regulation of p16CDKN2 expression and its implications for cell								
RT	immortalization and senescence."								
RL	Mol. Cell. Biol. 16:859-867(1996).								
RN	[4]								
RX	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.								
RX	MEDLINE=98421670; PubMed=9751050;								
RA	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;								
RT	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6								
RT	by the tumour suppressor p16INK4a."								
RL	Nature 395:237-243(1998).								
RN	[5]								
RX	REVIEW ON MELANOMA VARIANTS.								
RX	MEDLINE=96377761; PubMed=8783570;								
RA	Drapacoli N.C., Fountain J.W.;								
RT	"CDKN2 mutations in melanoma."								
RL	Cancer Surv. 26:115-132(1996).								
RN	[6]								
RX	REVIEW ON VARIANTS.								
RX	MEDLINE=96303699; PubMed=8723678;								
RA	Smith-Soerensen B., Hovig E.;								
RT	"CDKN2A (p16INK4A) somatic and germline mutations."								
RL	Hum. Mutat. 7:294-303(1996).								

ALIGNMENTS

RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
 RX MEDLINE=94338359; PubMed=8060323;
 RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
 RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41
 cell lung carcinomas.";
 RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
 [7]
 RP VARIANTS MELANOMA THR-49; SER-77; PRO-87; TRP-101; ASP-126 & THR-148.
 RX MEDLINE=95078916; PubMed=7987387;
 RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,
 ALly D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;
 RT "Germline p16 mutations in familial melanoma.";
 RL Nat. Genet. 8:15-21(1994).
 [9]
 RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.
 RX MEDLINE=95060835; PubMed=7970734;
 RA Zhou X., Tarmir L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
 Abraham J.M., Meltzer S.J.;
 RT "The MTS1 gene is frequently mutated in primary human esophageal
 tumors.";
 RL Oncogene 9:3737-3741(1994).
 [10]
 RP VARIANTS.
 RX MEDLINE=95188190; PubMed=7882351;
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
 Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,
 Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
 primary and metastatic lung cancer.";
 RL Cancer Res. 55:1448-1451(1995).
 [11]
 RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.
 RX MEDLINE=96121580; PubMed=8595405;
 RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,
 Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;
 RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma
 kindreds.";
 RL Hum. Mol. Genet. 4:1845-1852(1995).
 [12]
 RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
 RX MEDLINE=95375774; PubMed=7647780;
 RA Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,
 Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,
 Dracopoli N.C.;
 RT "Mutations associated with familial melanoma impair p16INK4
 function.";
 RL Nat. Genet. 10:114-116(1995).
 [13]
 RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.
 RX MEDLINE=96323259; PubMed=8710906;
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
 Luchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
 Isselbacher K.J., Sober A.J., Haber D.A.;
 RT "Prevalence of germline mutations in p16, p19ARF, and CDK4 in
 familial melanoma: analysis of a clinic-based population.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).
 [14]
 RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.
 RX MEDLINE=97472457; PubMed=9328469;
 RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,
 Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,
 Bishop D.T., Bishop J.N.;
 RT "Germline mutations of the CDKN2 gene in UK melanoma families.";
 RL Hum. Mol. Genet. 6:2061-2067(1997).
 [15]
 RP VARIANTS FAMILIAL MELANOMA.
 RX MEDLINE=98087572; PubMed=9425228;
 RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
 Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
 RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone
 families in France."

RL Hum. Mol. Genet. 7:209-216(1998).
 [16]
 RP Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
 Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
 RL Hum. Mol. Genet. 7:941-941(1998).
 [17]
 RP VARIANT PANCREATIC CARCINOMA CYS-146.
 RA Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,
 Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;
 RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple
 pancreatic carcinomas.";
 RL Hum. Mutat. 12:70-70(1998).
 [18]
 RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.
 RA Gretsardottir S., Olafsdottir G.H., Borg A.;
 RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,
 glioma and carcinoma of the pancreas.";
 RL Hum. Mutat. 12:212-212(1998).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
 ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
 REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
 CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
 CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
 WIDE RANGE OF TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 INHIBITORS.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L27211; AAA92554.1; -;
 DR EMBL; U12820; AAB60645.1; -;
 DR EMBL; U12818; AAB60645.1; JOINED.
 DR EMBL; U12819; AAB60645.1; JOINED.
 DR EMBL; S69804; AAD14048.1; -;
 DR EMBL; X94154; CAA63870.1; -;
 DR PUB; 1B77; 16-FEB-99.
 DR MIM; 600160; -;
 DR InterPro; IPR002110; -;
 DR Pfam; PF00023; ank; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;
 KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.
 FT REPEAT 11 40 ANK 1.
 FT REPEAT 44 72 ANK 2.
 FT REPEAT 77 106 ANK 3.
 FT REPEAT 110 139 ANK 4.
 FT VARIANT 14 14 D -> E (IN A BILIARY TRACT TUMOR).
 FT VARIANT 16 16 L -> P (IN A BILIARY TRACT TUMOR AND A
 FAMILIAL MELANOMA).
 FT /FTID=VAR_001408.
 FT /FTID=VAR_001409.
 FT A -> P (IN A LONG TUMOR AND MELANOMA).
 FT /FTID=VAR_001410.
 FT A -> S (IN A BILIARY TRACT TUMOR).
 FT /FTID=VAR_001411.
 FT G -> D (IN A PANCREAS TUMOR).
 FT /FTID=VAR_001412.
 FT R -> C (IN MELANOMA).
 FT /FTID=VAR_001413.
 FT R -> P (IN FAMILIAL MELANOMA AND
 MELANOMA).
 FT /FTID=VAR_001414.
 FT E -> D (IN A BILIARY TRACT TUMOR).
 FT /FTID=VAR_001415.
 FT L -> P (IN FAMILIAL MELANOMA).

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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:14:18 ; Search time 22.49 Seconds
(without alignments)
917.723 Million cell updates/sec

Title: US-09-016-869A-2
Perfect score: 156
Sequence: 1 MDPAGSMPEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : SPTREMBL_16.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_Organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_unclassified.*
 - 13: sp_vertebrate.*
 - 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	67.9	106	4	Q9NP05
2	54	34.6	81	6	Q9GME2
3	51	32.7	86	6	Q9XS52
4	51	32.7	102	6	Q9XS51
5	48	30.8	86	11	O54846
6	48	30.8	86	11	Q9Z1C1
7	48	30.8	86	11	Q9OUP0
8	47	30.1	103	6	Q9TSY1
9	32	20.5	36	4	Q9UPB7
10	32	20.5	116	4	Q95440
11	26	16.7	86	6	Q9TSY0
12	19	12.2	112	11	Q9QWH4
13	19	12.2	113	11	Q9Z1C2
14	19	12.2	159	11	Q9ROZ3
15	19	12.2	168	11	O89088
16	19	12.2	168	11	P97510
17	18	11.5	113	11	Q9QWH8
18	18	11.5	113	11	Q9QWH7
19	18	11.5	113	11	Q9QWH6

20	15	9.6	58	6	O97886	O97886 equus caball
21	15	9.6	113	11	Q9QWH5	Q9qwh5 mus musculus
22	14	9.0	21	4	Q9UD00	Q9ud00 homo sapien
23	12	7.7	157	11	Q9EQ33	Q9eq33 mesocricetu
24	8	5.1	44	11	Q9Z1C0	Q9z1c0 mus musculus
25	8	5.1	44	11	Q9QJ3	Q9qj3 mus musculus
26	8	5.1	91	14	Q9WLJ9	Q9wlj9 hepatitis e
27	8	5.1	124	13	P70067	P70067 xiphophorus
28	8	5.1	124	13	Q9W618	Q9w618 xiphophorus
29	8	5.1	300	14	P89468	P89468 herpes simp
30	8	5.1	334	1	O29818	O29818 archaeoglob
31	8	5.1	390	3	O94237	O94237 schizosacch
32	8	5.1	452	14	O71145	O71145 hepatitis e
33	8	5.1	487	14	O81869	O81869 hepatitis e
34	8	5.1	727	14	O81873	O81873 hepatitis e
35	8	5.1	747	14	O9J513	O9j513 fowlpox vir
36	8	5.1	1050	4	Q9H014	Q9h014 homo sapien
37	8	5.1	1205	3	Q9HFF5	Q9hff5 schizosacch
38	8	5.1	1685	14	Q9E8G6	Q9e8g6 hepatitis e
39	8	5.1	1693	14	Q69410	Q69410 hepatitis e
40	8	5.1	1693	14	O81344	O81344 hepatitis e
41	8	5.1	1693	14	O81862	O81862 hepatitis e
42	8	5.1	1693	14	O89444	O89444 hepatitis e
43	8	5.1	1693	14	O81876	O81876 hepatitis e
44	8	5.1	1693	14	O39221	O39221 hepatitis e
45	8	5.1	1693	14	Q9WLL5	Q9wll5 hepatitis e

ALIGNMENTS

RESULT 1

Q9NP05 ID Q9NP05 PRELIMINARY; PRT; 106 AA.

AC Q9NP05;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE CDK4I PROTEIN (FRAGMENT).

GN CDK4I.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94203288; PubMed=8152487;

RA Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.;

RT "Deletions of the cyclin-dependent kinase-4 inhibitor gene in multiple human cancers."

RL Nature 368:753-756(1994).

DR EMBL; S69824; AAD14050.1; .

DR EMBL; S69822; AAD14050.1; JOINED.

DR InterPro: IPR002110; .

DR Pfam: PF00023; ank; 1.

DR PROSITE; PS50297; ANK_REP_REGION; 1.

FT NON_TER 1

SQ SEQUENCE 106 AA; 11314 MW; 2D59442F956B6A61 CRC64;

Query Match 67.9%; Score 106; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.7e-92;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	51	VMMGSRVAEELLLHGAEPNCADPATLTPVHDAAREGFLDPLVVLHVRAGALDVRDAM	110
Db	1	VMMGSRVAEELLLHGAEPNCADPATLTPVHDAAREGFLDPLVVLHVRAGALDVRDAM	60
QY	111	GRLPVDLAEELGHROVARYLRAAAGTGTSNHNARIDAAEGPSDIPD	156
Db	61	GRLPVDLAEELGHROVARYLRAAAGTGTSNHNARIDAAEGPSDIPD	106

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RESULT 2
Q9GMF2 PRELIMINARY; PRT; 81 AA.
AC Q9GMF2;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Venkatraj V.S., Mayor J., Modiano J.F.;
RT "Role of p16/Ink4-a in familial canine cancers.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234176; AAG01087.1; -.
KW Kinase.
SQ SEQUENCE 81 AA; 8668 MW; 0E39D8D805BEAC0F CRC64;
Query Match 34.6%; Score 54; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 77 TLRPVDHAAAREGFDTLVVHLHRAGALDVRDAGRLPVDLAEEELGHRDVARYL 130
DB 27 TLRPVDHAAAREGFDTLVVHLHRAGALDVRDAGRLPVDLAEEELGHRDVARYL 80
RESULT 3
Q9XS52 PRELIMINARY; PRT; 86 AA.
AC Q9XS52;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RA Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010808; BAA33541.1; -.
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 2.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT NON_TER 1
SQ SEQUENCE 86 AA; 9340 MW; A59FF0193290E867 CRC64;
Query Match 32.7%; Score 51; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 PNCADPATLTRPVHDAAREGFDTLVVHLHRAGALDVRDAGRLPVDLAEE 120
DB 20 PNCADPATLTRPVHDAAREGFDTLVVHLHRAGALDVRDAGRLPVDLAEE 70
RESULT 4
Q9XS51 PRELIMINARY; PRT; 102 AA.
AC Q9XS51;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RA Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -.
DR HSSP; P42771; 1B17.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 3.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT NON_TER 1
SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;
Query Match 32.7%; Score 51; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.5e-40;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 PNCADPATLTRPVHDAAREGFDTLVVHLHRAGALDVRDAGRLPVDLAEE 120
DB 20 PNCADPATLTRPVHDAAREGFDTLVVHLHRAGALDVRDAGRLPVDLAEE 70
RESULT 5
Q54846 PRELIMINARY; PRT; 86 AA.
AC Q54846;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Malumbres M., Pellicer A.;
RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF015460; AAB94534.1; -.
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; -.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT NON_TER 1
SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;
Query Match 30.8%; Score 48; DB 11; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.5e-37;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 VAEILLHGAEPNCADPATLTRPVHDAAREGFDTLVVHLHRAGALDV 106
DB 9 VAEILLHGAEPNCADPATLTRPVHDAAREGFDTLVVHLHRAGALDV 56
RESULT 6
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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:06:13 ; Search time 19.51 Seconds
(without alignments)
484.743 Million cell updates/sec

Title: US-09-016-869A-2
Perfect score: 156
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	156	100.0	156	16 AAR85116	Cell-cycle regulat
2	156	100.0	156	20 AAY24741	Human INK-4 protei
3	156	100.0	156	21 AAY88354	Human cell cycle r
4	153	98.1	391	18 AAW23534	CDK inhibitory fus
5	153	98.1	391	20 AAW95094	Human p27-p16 fusi
6	153	98.1	391	21 AAY97526	Human W3 protein s
7	153	98.1	391	21 AAY96041	Antiproliferative
8	153	98.1	391	21 AAY96068	Angiogenesis inhib
9	148	94.9	148	16 AAR81701	Multiple tumour su
10	148	94.9	148	16 AAR80940	Human multiple tum
11	148	94.9	151	15 AAR53401	Inhibitor of cycli

12	121	77.6	156	18 AAW10627	Tumour suppressor
13	121	77.6	156	18 AAW19251	Human multiple tum
14	121	77.6	156	19 AAW74549	Amino acid sequenc
15	121	77.6	156	19 AAW40524	Human MTS1 protein
16	121	77.6	156	20 AAW80524	A human multiple t
17	121	77.6	156	21 AAB15498	Human MTS1 protein
18	121	77.6	156	21 AAY97524	Human p16 protein
19	121	77.6	156	21 AAY96053	Human cyclin depen
20	121	77.6	156	21 AAY96067	Human cyclin depen
21	121	77.6	156	21 AAY92921	Human multiple tum
22	121	77.6	156	21 AAY91102	Human multiple tum
23	121	77.6	156	21 AAY59415	Human MTS1 protein
24	121	77.6	156	21 AAY54902	Human multiple tum
25	121	77.6	156	22 AAB67334	Protein encoded by
26	121	77.6	156	22 AAB67390	Human Multiple Tum
27	121	77.6	228	21 AAY97522	Human W9 protein s
28	121	77.6	228	21 AAY96051	Antiproliferative
29	121	77.6	228	21 AAY96078	Angiogenesis inhib
30	121	77.6	237	20 AAW95105	Truncated p27/p16
31	121	77.6	237	21 AAY97534	Human W9 protein s
32	121	77.6	237	21 AAY96049	Antiproliferative
33	121	77.6	237	21 AAY96076	Angiogenesis inhib
34	121	77.6	252	20 AAW95106	Truncated p27/p16
35	121	77.6	252	21 AAY97535	Human W10 protein
36	121	77.6	252	21 AAY96050	Antiproliferative
37	121	77.6	252	21 AAY96077	Angiogenesis inhib
38	121	77.6	323	21 AAY96079	Secretable angio
39	121	77.6	334	20 AAW95103	Truncated p27/p16
40	121	77.6	334	21 AAY97532	Human W8 protein s
41	121	77.6	334	21 AAY96047	Antiproliferative
42	121	77.6	334	21 AAY96074	Angiogenesis inhib
43	121	77.6	365	18 AAW23536	CDK inhibitory fus
44	121	77.6	365	20 AAW95107	Human p16p27 fusi
45	121	77.6	365	20 AAW95096	Human p16p27 fusi

ALIGNMENTS

RESULT 1
AAR85116
ID AAR85116 standard; Protein; 156 AA.
XX AAR85116;
AC AAR85116;
XX 01-MAR-1996 (first entry)
XX Cell-cycle regulatory protein p16.
XX Cell-cycle regulatory protein p16.
XX Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
XX CCR; cancer; cell proliferation.
XX Homo sapiens.
XX WO9528483-A1.
XX 26-OCT-1995.
XX 14-APR-1995; 95WO-US04636.
XX 29-NOV-1994; 94US-0346147.
XX 14-APR-1994; 94US-0227371.
XX 25-MAY-1994; 94US-0248812.
XX 14-SEP-1994; 94US-0306511.
XX (COLD-) COLD SPRING HARBOR LAB.
XX Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
XX WPI; 1995-373798/48.
XX N-PSDB; AAT02962.
XX New cell cycle regulating proteins bind to cyclin dependent kinase -

PT and related nucleic acids, antibodies etc., used in diagnosis and
PT therapy of abnormal cell proliferation, degeneration etc.
XX
PS
XX Claim 1; Page 76-77; 109pp; English.
XX
CC The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was
CC obtd. by expression of a cDNA clone (AAT02962) isolated in a 2-hybrid
CC screening assay. CCR p16 specifically inhibits the activity of
CC cyclin-dependent kinases during various stages of the cell cycle,
CC and can be used in the treatment and diagnosis of proliferative
CC disorders.
XX
SQ Sequence 156 AA;

Query Match 100.0%; Score 156; DB 16; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.2e-141;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRP10VMMGSAARVA 60
Db 1 mdpagssmepsadwlataaargveevrllleavlpnapnsygrripqvmmgssarva 60
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
Qy 61 ellllhgaepncadpatltrpvhdaaregfldtlvvlrharagldvdrdagrldpvdlaee 120
Db 61 ellllhgaepncadpatltrpvhdaaregfldtlvvlrharagldvdrdagrldpvdlaee 120
Qy 121 LGHRDVARYLRAAGGTRGSHNARIDAAGPSDIPD 156
Db 121 lghrdvarylraaaggtrgsnharidaaegpsdipd 156

-RESULT 2
AAV24741
ID AAY24741 standard; Protein: 156 AA.
XX
AC AAY24741;
XX
DT 23-AUG-1999 (first entry)
XX
DE Human INK-4 protein p16.
XX
XX INK-4; p16; p18; p19; CDK4; cell cycle regulatory protein;
KW transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.
XX
XX Homo sapiens.
XX
XX US5919997-A.
PD 06-JUL-1999.
XX
XX 04-APR-1996; 96US-0627610.
XX
XX 04-APR-1996; 96US-0627610.
PR 18-NOV-1993; 93US-0154915.
PR 14-APR-1994; 94US-0227371.
PR 25-MAY-1994; 94US-0248812.
PR 14-SEP-1994; 94US-0306511.
PR 29-NOV-1994; 94US-0346147.
PR 30-JUN-1995; 95US-0497214.
PR 02-JAN-1996; 96US-0361918.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
XX Beach DH, DePinho RA, Serrano M;
XX
XX WPI; 1999-394656/33.
DR N-PSDB; AAX80472.
XX
XX Transgenic mice with modified cell-cycle regulation
XX
XX Disclosure; Column 45-46; 35pp; English.

XX The present invention describes a transgenic mouse having germline and
CC somatic cells which comprise an incorporated transgene that disrupts and
CC inhibits the p16-INK4-a gene leading to tumour susceptibility. Also
CC described is a method of making a mouse and mouse embryonic stem cells a
CC functionally disrupted p16-INK4-a gene which comprises transferring a
CC transgene construct into mouse embryonic stem cells of a mouse and
CC transferring these into a mouse blastocyst and implanting the resulting
CC chimeric blastocyst into a female mouse selecting offspring having an
CC endogenous p16-INK4-a gene allele. The transgenic mouse is useful for
CC evaluating the carcinogenic potential or the anti-proliferative activity
CC of a test compound. The present sequence represents the human INK4
XX protein p16 given in the present invention.
SQ Sequence 156 AA;

Query Match 100.0%; Score 156; DB 20; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.2e-141;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRP10VMMGSAARVA 60
Db 1 mdpagssmepsadwlataaargveevrllleavlpnapnsygrripqvmmgssarva 60
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
Qy 61 ellllhgaepncadpatltrpvhdaaregfldtlvvlrharagldvdrdagrldpvdlaee 120
Db 61 ellllhgaepncadpatltrpvhdaaregfldtlvvlrharagldvdrdagrldpvdlaee 120
Qy 121 LGHRDVARYLRAAGGTRGSHNARIDAAGPSDIPD 156
Db 121 lghrdvarylraaaggtrgsnharidaaegpsdipd 156

RESULT 3
AAV88354
ID AAY88354 standard; Protein: 156 AA.
XX
AC AAY88354;
XX
DT 14-JUL-2000 (first entry)
XX
DE Human cell cycle regulatory protein p16 amino acid sequence.
XX
XX Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection;
KW cell proliferation; differentiation; neoplasia; cancer; cell growth;
KW cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.
XX
XX Homo sapiens.
XX
XX US6043030-A.
PN
XX 28-MAR-2000.
PD
XX 02-JAN-1996; 96US-0581918.
XX
XX 17-DEC-1992; 92US-0991997.
PR 18-NOV-1993; 93US-0154915.
PR 14-APR-1994; 94US-0227371.
PR 25-MAY-1994; 94US-0248812.
PR 14-SEP-1994; 94US-0306511.
PR 29-NOV-1994; 94US-0346147.
PR 30-JUN-1995; 95US-0497214.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX Beach DH, Demetrick DJ, Serrano M, Hannon GJ;
XX
XX WPI; 2000-270336/23.
DR N-PSDB; AAA13096.
XX
XX Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory
PT protein) in a diagnostic assay for identifying a cell at risk for a

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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:02:33 ; Search time 70.99 seconds
(without alignments)
167.393 Million cell updates/sec

Title: US-09-016-869A-2
Perfect score: 800
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	789	98.6	156	2 JE0141	cyclin dependent k
2	529	66.1	130	2 I78845	p15INK4b - mouse
3	526	65.8	138	2 B55479	CDK4 inhibitor p14
4	461.5	57.7	167	2 I58352	p16INK4a - mouse
5	358	32.2	164	2 A57378	cyclin-dependent k
6	249	31.1	166	2 A57379	CDK4/CDK6 inhibito
7	244	30.5	166	2 B57378	cyclin-dependent k
8	231.5	28.9	168	2 B57379	CDK4/CDK6 inhibito
9	228.5	28.6	168	2 A55479	CDK6 inhibitor p18
10	209	26.1	41	2 I52720	gene p15INK4B prot
11	158	19.8	3924	2 S37431	ankyrin 2, neurona
12	137.5	17.2	1848	2 S37771	ankyrin, erythrocy
13	137.5	17.2	1862	2 I49502	ankyrin - mouse
14	133.5	16.7	1856	2 B35049	ankyrin 1, erythro
15	133.5	16.7	1880	2 A35049	ankyrin 1, erythro
16	133.5	16.7	1881	1 S7HUK	ankyrin 1, erythro
17	131	16.4	857	2 G62694	potassium channel
18	130.5	16.3	1423	1 I37275	death-associated p
19	130	16.2	838	2 S23606	potassium channel
20	130	16.2	1765	2 T42714	ankyrin 3, splice
21	130	16.2	1940	2 T42715	ankyrin 3, splice
22	130	16.2	1943	2 T42713	ankyrin 3, splice
23	130	16.2	1961	2 T42716	ankyrin 3, splice
24	128	16.0	4377	2 A55575	ankyrin 3, long sp
25	127.5	15.9	1786	2 A57282	ankyrin-related pr
26	127.5	15.9	1815	2 T15346	elegans ankyrin-re
27	127.5	15.9	1867	2 T15344	ankyrin-related un
28	127.5	15.9	2039	2 T15347	ankyrin-related un
29	126	15.8	247	2 D84448	probable ankyrin [

30 125 15.6 1964 2 T09059 notch4 - mouse
31 124.5 15.6 209 2 T5888 hypothetical prote
32 121 15.1 237 2 T50984 related to 26s pro
33 121 15.1 888 2 D84650 probable potassium
34 120 15.0 476 2 T23213 hypothetical prote
35 118.5 14.8 347 2 C40858 GA-binding protein
36 118.5 14.8 382 2 B40858 GA-binding protein
37 117.5 14.7 347 2 C48146 nuclear respirator
38 117.5 14.7 348 2 I38744 nuclear respirator
39 117.5 14.7 360 2 I38743 nuclear respirator
40 117.5 14.7 395 2 I38741 nuclear respirator
41 117 14.6 1435 2 T32930 hypothetical prote
42 116.5 14.6 1031 2 T43458 hypothetical prote
43 116 14.5 1549 2 T13940 ankyrin - fruit fl
44 115.5 14.4 1058 2 D82654 ankyrin-like prote
45 114 14.2 828 2 T52046 potassium channel

ALIGNMENTS

RESULT 1
JE0141
cyclin dependent kinase inhibitor - human
N:Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor
C:Species: Homo sapiens (man)
C>Date: 02-Jun-1998 #sequence.revision 10-Jul-1998 #text_change 19-May-2000
C:Accession: JE0141; I59268; S39359; I59585; JC5679
R:Huang, C.G.; Deng, W.; Fu, J.L.
Chin, J. Biotechnol. 13, 105-107, 1997
A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.
A:Reference number: JE0141
A:Accession: JE0141
A:Molecule type: mRNA
A:Residues: 1-156 <HUA>
A:Experimental source: Hella cell
R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Haglward, K.; Hussain, S.P.; Bennett, Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994
A:Title: Mutations and altered expression of p16INK4 in human cancer.
A:Reference number: I59268; MUID:95062202
A:Accession: I59268
A>Status: translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-152 <OKA>
A:Cross-references: GB:L27211; NID:G558656; PIDN:AAA92554.1; PID:G558657
A:Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AAA925
R:Serrano, M.; Hannon, G.J.; Beach, D. Nature 366, 704-707, 1993
A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of
A:Reference number: S39359; MUID:94081956
A:Accession: S39359
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 9-34, 'V', 36-156 <SEB>
A:Note: this sequence is corrected in reference I59268
R:Kamb, A.; Grusis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Science 264, 436-440, 1994
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.
A:Reference number: I59585; MUID:94204645
A:Accession: I59585
A>Status: translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 51-152 <KAM>
A:Cross-references: GB:S69804; NID:G546272; PIDN:AAAD14048.1; PID:G4261748
C:Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 k1
C:Genetics:
A:Gene: GDB:CDKN2A; CDK4I; MLM; P16; INK4; MTS1; CMM2; CDKN2
A:Cross-references: GDB:335362; OMIM:600160
A:Map position: 9p21-9p21
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

```

Query Match      57.78; Score 461.5; DB 2; Length 167;
Best Local Similarity 63.28; Pred. No. 4.7e-36;
Matches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;

QY          9  MEPSADWLATAAARGVEEVREALLAEVALNPNSTCYRRPIQVMMMSGARVAELLHLHGA 68
               ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
db           1  MESAADRLLA-AAAGRGVHDVRALLAEACGVSNAFNSFGRTPIQVMMGNVHVAAELNLGTA 59
               ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY      69  EPNCADPATLRPVHDAAREGFDTLVLHFRAGARLDVRDAGRLPVDLAEEIGHRDVAR 128
      :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      60  DSNCEDPTTFSRPVHDAAREGFDTLVLHFRSGARLDVRDAGRLPDLDAQERGHODIVR 119

```

QY 129 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155
|||:| ||: | |: | | |
Db 120 YLRAGCSLC SAGWSLCTAGNVAOTDGHFSSTP 154

RESULT
A57378
5

A:Species: Homo sapiens (man)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
C:accession: A57378
R:Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
Mol. Cell. Biol. 15, 2682-2688, 1995
A:title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor
A:Reference number: A57378; MUID:95257949
A:Accession: A57378
P:Accession: A57378
A:Molecule type: mRNA
A:Residues: 1-164 <CHA>
A:Cross-references: GB:U20498
C:Genetics:
A:Map position: 19p13
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology;

Query Match 32.2%; Score 258; DB 2; Length 164;
Best Local Similarity 44.1%; Pred. No. 4.8e-17;
Matches 67; Conservative 17; Mismatches 62; Indels 6; Gaps 3;

Qy 10 EPSADWLATAAAARGVVEVRALL-EAVALPNAPNSYGRRIQIVMMGMSARVAELLHLGA 68
+ + :
Dd 5 EVRAGTLSGAAARGDVQEVRRLLHRELVHPDALNRFKGTALQVMVFGSTALELLKOGA 64

Qy 69 EPNCADPATLTPRVHDAAREGFDTLVLLHRAGARLDVDRDANGRLPVDLAEELCHRDVAR 128
 || | : | ||||| ||||| || | :: | || : | : |
Dd 65 SPINODTSG-TSPYHDAARTGFTDPIKVLVRHGADVNPDCGTGALPIHTAVOEGHTAVVS 123
 || | : | ||||| ||||| || | :: | || : | : |

QY 129 YLRAAG----GTRGSNHARIDAAEGPSDIPD 156
:| |:| |:| |:| |:| |:|
Db 124 FLAASDLHRRDARGLTPLELAIORGAODLVD 155

RESULT
A57370
6

C:Accession: A57379
 C:Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the c
 A:Reference number: A57379; MUID:95257948
 A:Accession: A57379
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-166 <HIR>
 A:Cross-references: GB:U19597; NID:g790568; PIDN:AC52194.1; PID:g790569
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
 C:Keywords: cell cycle control

Query Match 31.1%; Score 249; DB 2; Length 166;
Best Local Similarity 44.3%; Pred. No. 3.4e-16;
Matches 70; Conservative 18; Mismatches 52; Indels 18; Gaps 5;

QY 14 DWLATAARGVEEVRALL-EAVALPNAPNSYGRRPQVMMNGSARVAELLILHGAEPNC 72
| | : | | | | | : | : | : | : | | | | | | | |
Dbb 10 DRLSGARAGDVOEVRELLHRELIVHPDALNRFGTALQVMVGSPAVALELLKOGASPNV 69

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Qy 73 ADPATLTRPVHDAAREGFDTLVLHRAGARLDVDRDAGRLPVDLAEECHRDVARYL-- 130
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 70 QD--ASGTSVPHDAARTGFDTLVKLVVEHGADYNALDSTGSLPHLAIREGHSSVVSFLAP 128

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Qy 131 -----RAAAGGT-----RGSNHARIDAAEGPSDIP 155
      | | | | | | | | | | | | | | | | | |
Db 129 ESDIHRDASGLTPUELARORGAONLMDILOGHMMIP 165

```

RESULT
B57378
7

B57378
cyclin-dependent kinase inhibitor p19 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999
C:Accession: B57378
R:Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
Mol. Cell. Biol. 15, 2682-2688, 1995
A:Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with
A:Reference number: A57378; MUID:95257949
A:Accession: B57378
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166 <CHA>
A:Cross-references: GB:U20497; NID:g791204; PID:AAA85437.1; PID:g791205
C:Superfamily: unassigned ankryin repeat proteins; ankryin repeat homolog; EGF homolog

Query Match 30.5%; Score 244; DB 2; Length 166;
Best Local Similarity 43.7%; Pred. No. 9.8e-16;
Matches 69; Conservative 18; Mismatches 53. Indels

QY 14 DWLATAAARGVEEVALL-EAVALPNA²NSYGR²RP²IQVMMG²SARVAE²LL²LLHCAEPNC 72

db 10 DR²LSARPRG²VD²EV²RL²HREL²VHPD²AL²NRE²GK²ALOV²MF²GSP²AVALE²LLKQASPNV 69

QY 73 ADPATLTPRVHDAAREGFLOTLVILHRAGARLDVRDAGRPLPVDIAEELGHRDVAYLL - 130
- : | | | | | | | | | | : : | | : | : | : |
dh 70 QD-A-SGTSPVHDAARTGFLOTKVIVHGADVNALDTGSLPTHTATREGSSVVWFLAP 128

```

QY 131 -----RAAGGT-----RGSNHARIDAAEGPSDIP 155
      | | | | | || : : : | |
DY 120 ESNIHUBDASCIITDITAPDQCAONI-MDTIOCHUMMID 165

```

RESULT
DE7370
8

B57379
CDK4/CDK6 inhibitor p18 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999
C:Accession: B57379
R:Hirai, H.; Rousset, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.
Mol. Cell. Biol. 15, 2672-2681, 1995
A:Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinase
A:Reference number: A57379; MUID:95257948
A:Accession: B57379
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-168 <HR>
A:Cross-references: GB:U19596; NID:g790566; PID:AAC52193.1; PID:g790567
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C:Keywords: cell cycle control

Query Match	28.9%;	Score 231.5;	DB 2;	Length 168;
Best Local Similarity	40.3%;	Pred. No. 1.5e-14;		
Matches 56;	Conservative	22;	Mismatches 60;	Indels 1

QY 10 EPSADWLATAAARGRVEEVRALLAEVALPNAPNSYGRPIQVMMGMSARVAELLHLHGAEE699
 || : ||:||||| : :: ||: || : || : ||: ||: ||: : || : |||| ||
db 3 EPWGHIELASAAARGDLEGTSLLONNVNVAONGFETALOVNKLGNPETARRLLRGAN62

QY 70 PNCADPATILTRPVHDAAREGFLDTLVLHHRAGARLDVRDAWGRLPVDLAEELGHRDVARY

RN RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
 RX MEDLINE-94338359; PubMed-8060323;
 RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
 RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41
 (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small
 cell lung carcinomas.";
 RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
 [8]
 RN RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.
 RX MEDLINE-95078916; PubMed-7987387;
 RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,
 RT Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;
 RL "Germline p16 mutations in familial melanoma.";
 RN Nat. Genet. 8:15-21(1994).
 [9]
 RN RP VARIANTS SOUMAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.
 RX MEDLINE-95060835; PubMed-7970734;
 RA Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
 RT Abraham J.M., Melitzer S.J.;
 RL "The MTS1 gene is frequently mutated in primary human esophageal
 tumors.";
 RN Oncogene 9:3737-3741(1994).
 [10]
 RN RP VARIANTS
 RX MEDLINE-95188190; PubMed-7882351;
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
 RT Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;
 RL "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
 primary and metastatic lung cancer.";
 RN Cancer Res. 55:1448-1451(1995).
 [11]
 RN RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.
 RX MEDLINE-96121580; PubMed-8595405;
 RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,
 RT Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;
 RL "Mutations of the CDKN2/p16INK4 gene in Australian melanoma
 kindreds.";
 RN Hum. Mol. Genet. 4:1845-1852(1995).
 [12]
 RN RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
 RX MEDLINE-95375774; PubMed-7647780;
 RA Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,
 RT Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,
 RL Dracopoli N.C.;
 RT "Mutations associated with familial melanoma impair p16INK4
 function.";
 RN Nat. Genet. 10:114-116(1995).
 [13]
 RN RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.
 RX MEDLINE-96323259; PubMed-8710906;
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
 RT Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
 RL Isselbacher K.J., Sober A.J., Haber D.A.;
 RT "Prevalence of germline mutations in p16, p19ARF, and CDK4 in
 familial melanoma: analysis of a clinic-based population.";
 RN Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).
 [14]
 RN RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.
 RX MEDLINE-97472457; PubMed-9328469;
 RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,
 RT Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,
 RL Bishop D.T., Bishop J.N.;
 RT "Germline mutations of the CDKN2 gene in UK melanoma families.";
 RN Hum. Mol. Genet. 6:2061-2067(1997).
 [15]
 RN RP VARIANTS FAMILIAL MELANOMA.
 RX MEDLINE-98087572; PubMed-9425228;
 RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombléd J.,
 RT Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
 RL "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone
 families in France."

Hum. Mol. Genet. 7:209-216(1998).
 [16]
 RN ERRATUM.
 RP Soufir N., Avril M.-F., Chompret A., Demenais F., Bombléd J.,
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
 RN Hum. Mol. Genet. 7:941-941(1998).
 [17]
 RN RP VARIANT PANCREATIC CARCINOMA CYS-146.
 RA Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,
 RA Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;
 RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple
 pancreatic carcinomas.";
 RN Hum. Mutat. 12:70-70(1998).
 [18]
 RN RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.
 RA Gretsardottir S., Olafsdottir G.H., Borg A.;
 RT glioma and carcinoma of the pancreas.";
 RN Hum. Mutat. 12:212-212(1998).
 CC - FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
 ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
 REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
 CC - SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
 CC - DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
 WIDE RANGE OF TISSUES.
 CC - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 INHIBITORS.
 CC - SIMILARITY: CONTAINS 4 ANK REPEATS.
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 EMBL; L27211; AAA92554.1; -
 DR EMBL; U12820; AAB60645.1; -
 DR EMBL; U12818; AAB60645.1; JOINED.
 DR EMBL; U12819; AAB60645.1; JOINED.
 DR EMBL; S69804; AAD14048.1; -
 DR EMBL; X94154; CAA63870.1; -
 DR PDB; 1BI7; 16-FEB-99.
 DR MIM; 600160; -
 DR InterPro; IPR002110; -
 DR Pfam; PF00023; ank; 3.
 DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
 DR Cell Cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;
 KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.
 FT REPEAT 11 40 ANK 1.
 FT REPEAT 44 72 ANK 2.
 FT REPEAT 77 106 ANK 3.
 FT REPEAT 110 139 ANK 4.
 FT VARIANT 14 14 D -> E (IN A BILIARY TRACT TUMOR).
 FT VARIANT 16 16 L -> P (IN A BILIARY TRACT TUMOR AND A
 FAMILIAL MELANOMA).
 FT VARIANT 20 20 A -> P (IN A LONG TUMOR AND MELANOMA).
 FT VARIANT 20 20 A -> S (IN A BILIARY TRACT TUMOR).
 FT VARIANT 23 23 G -> D (IN A PANCREAS TUMOR).
 FT VARIANT 24 24 R -> C (IN MELANOMA).
 FT VARIANT 24 24 R -> P (IN FAMILIAL MELANOMA AND
 MELANOMA).
 FT VARIANT 26 26 E -> D (IN A BILIARY TRACT TUMOR).
 FT VARIANT 32 32 L -> P (IN FAMILIAL MELANOMA).

Query Match 98.6%; Score 789; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 3.5e-66;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLTAAAGRVVEEVALLEAVALNPNSYGRRPITQVMMGSAVA 60
 Db 1 MEPAAGSSMEPSADWLTAAAGRVVEEVALLEAVALNPNSYGRRPITQVMMGSAVA 60

QY 61 LGGHVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRWAGRLPVDLAE 120

QY 121 LGGHVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
 Db 121 LGGHVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 2
 CDN5_MOUSE STANDARD; PRT; 130 AA.

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
 GN CDKN2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95380169; PubMed=7651726;
 RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
 RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
 RT "Cloning and characterization of murine p16INK4a and p15INK4b genes";
 RL Oncogene 11:635-645(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J X DBA;
 RX MEDLINE=973222242; PubMed=9178896;
 RA Malumbres M., de Castro I., Santos J., Melendez B., Manges R.,
 RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
 RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by
 deletion and de novo methylation with independence of p16INK4a
 alterations in murine primary T-cell lymphomas";
 RL Oncogene 14:1361-1370(1997).
 RP -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
 CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
 CC SIMILARITY).
 CC -!- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
 CC -!- INDUCTION: BY TGF-BETA.
 CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 CC INHIBITORS.
 CC -!- SIMILARITY: CONTAINS 4 ANK REPEATS.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U66085; AAB39833.1; -
 DR EMBL; U66084; AAB39833.1; JOINED.
 DR MGD; MGI:104737; Cdkn2b.
 DR InterPro; IPR002110; -
 DR Pfam; PF00203; ank; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.

Cell cycle; Anti-oncogene; Repeat; ANK repeat.
 FT REPEAT 5 34 ANK 1.
 FT REPEAT 38 66 ANK 2.
 FT REPEAT 71 100 ANK 3.
 FT REPEAT 104 130 ANK 4.
 SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF552BCFF9 CRC64;

Query Match 66.1%; Score 529; DB 1; Length 130;
 Best Local Similarity 88.3%; Pred. No. 2.8e-42;
 Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 16 LATAAARGVVEEVALLEAVALNPNSYGRRPITQVMMGSAVAELLLHGAEPNCADP 75
 Db 10 LATAAARGVETVRLLEAGADNALNRFRPITQVMMGSAVAELLLHGAEPNCADP 69

QY 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRWAGRLPVDLAEELGHRDVARYLRAAAG 135
 Db 70 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVCDWAGRLPVDLAEEOGHRDIARYLHAAYG 129

RESULT 3
 CDN5_HUMAN STANDARD; PRT; 138 AA.

AC P42772;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
 DE (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
 GN CDKN2B OR MTS2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95095079; PubMed=8001816;
 RA Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
 RA Matera G.A., Xiong Y.;
 RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
 RT CDK6 inhibitor, correlates with wild-type pRb function";
 RL Genes Dev. 8:2939-2952(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359613; PubMed=8078588;
 RA Hannon G.J., Beach D.;
 RT "p15INK4B is a potential effector of TGF-beta-induced cell cycle
 RT arrest";
 RL Nature 371:257-261(1994).
 RN [3]
 RP SEQUENCE OF 53-138 FROM N.A.
 RX MEDLINE=94204645; PubMed=8153634;
 RA Kamb A., Gius N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
 RA Tavtigian S.V., Stockert E., Bay R.S. III, Johnson B.E.,
 RA Skolnick M.H.;
 RT "A cell cycle regulator potentially involved in genesis of many tumor
 RT types";
 RL Science 264:436-440(1994).
 RN [4]
 RP VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.
 RX MEDLINE=95188190; PubMed=7882351;
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
 RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,
 RA Xiong Y., Beach D.H., Yokota J., Harris C.C.;
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
 RT primary and metastatic lung cancer";
 RL Cancer Res. 55:1448-1451(1995).
 CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
 CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.
 CC -!- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
 CC -!- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
 CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE

```
Cancer Res. 55:1607-1612(1995).
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY SIMILARITY).
-!- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
-!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN TESTIS, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.
-!- SIMILARITY: CONTAINS 4 ANK REPEATS.
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EMBL; S79760; AAB35360.1; -.
EMBL; S77734; -, NOT_ANNOTATED_CDS.
InterPro: IPR002110; -.
Pfam: PF00023; ank; 3.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REP_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
FT CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B, LONG ISOFORM.
FT FT CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B, SHORT ISOFORM.
FT FT INIT_MET 46 46 FOR SHORT ISOFORM.
FT FT REPEAT 5 34 ANK 1.
FT FT REPEAT 38 66 ANK 2.
FT FT REPEAT 71 100 ANK 3.
FT FT REPEAT 104 130 ANK 4.
FT SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

Query Match          65.5%; Score 524; DB 1; Length 130;
Best Local Similarity 86.7%; Pred No. 8e-42;
Matches 104; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 16 LATAAARGVEEVREALLAEVALPNAPNSGYRRPIQVMMGMSARVAELLLHGASPNCADP 75
      |||||   ||| | | | | :|||||:|||||:|||||:|||||:|||||:|||||:
DB 10 LATAAARGQVETVRQLLEAGADPNANVRGRPRIQVMMGSAQAELLLHGASPNCADP 69
      |||||   ||| | | | | :|||||:|||||:|||||:|||||:|||||:|||||:

QY 76 ATLTRPVHDAAAREGEFLDTLVLRHAGARDLDVDWAGRLPDVLAEEGLHRDVARVYLRAAAG 135
      |||||   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 70 ATLTRPVHDAAAREGEFLDTLMVLHKAGARDLCDWAGRLPDVLAEBEQGHDIARYLHAATG 129

RESULT 5
CDN2_MOUSE
ID CDN2_MOUSE STANDARD; PRT; 167 AA.
AC P51480;
DC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DD 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A).
GN CDKN2A OR P16INK4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95380169; PubMed=7651726;
RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.:
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
```

	-!- SIMILARITY: CONTAINS 2 ANK REPEATS.
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CC	EMBL; U17075; AAC50075.1; --
DR	EMBL; L36844; AAA50282.1; --
CC	EMBL; S69805; AAD14049.1; --
DR	MIM; 600431; --
DR	PROSITE; PS50297; ANK_REP_REGION; 1.
KW	Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation.
FT	REPEAT_13..39 ANK 1 (INCOMPLETE).
FT	REPEAT_73..103 ANK 2.
FT	VARIANT_47..47 G->E (IN LUNG ADENOCARCINOMA).
CC	/FTID-VAR_001488.
DR	A->V (IN LUNG ADENOCARCINOMA).
CC	/FTID-VAR_001489.
FT	SATISFACTION SA->TP (IN REF. 2).
FT	CONFLICT_23..23 MISSING (IN REF. 2).
FT	CONFLICT_32..34 QLL->HSW (IN REF. 2).
CC	SEQUENCE 138 AA; 14722 MW; OD6FFBDEAFED21 CRC64;
CC	Query Match 65.8%; Score 526; DB 1; Length 138;
CC	Best Local Similarity 82.0%; Pred. No. 5.6e-42;
CC	Matches 109; Conservative 4; Mismatches 16; Indels 4; Gaps 1;
OY	3 PAAGSMPEFSDWLATAAARGVEEVALLAEVALPNAPNSYGRRPIQVMNGSARVAEL 62
DB	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
DB	9 PGGSGDS-----GLSAAGALGVLEKVQLLEGADPNGVNRFGRAIQIIVMMGARSARVAEL 64
OY	63 LLHGAEPNCADPATLPTRPVHDAAAREGFDTLVVLHRAGARDLRDANGRLPVDLAEEIG 122
DB	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
DB	65 LLHGAEPNCADPATLPTRPVHDAAAREGFDTLVVLHRAGARDLRDANGRLPVDLAEEERG 124
OY	123 HRDVARYURAAAG 135
DB	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :
DB	125 HRDVAYGLRTATG 137
RESULT 4	
CDC5_RAT	STANDARD; PRF; 130 AA.
P5272;	
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
GN	CDKN2B OR INK4.
OS	Rattus norvegicus (Rat).
CS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxId=10116;	[1]
RP	SEQUENCE FROM N.A.
PP	MEDLINE=96001392; PubMed=7546221;
RX	Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
RA	Tsuchiya H., Kikuchi Y., Mitani H.;
RA	"Molecular genetic basis of renal carcinogenesis in the Eker rat
RT	model of tuberosus sclerosis (Tsc2).";
RL	Mol. Carcinog. 14:23-27(1995).
RN	[2].
RP	SEQUENCE OF 46-86 FROM N.A.
RX	MEDLINE=95228036; PubMed=7712460;
RA	Knapsek D.F., Serrano M., Beach D., Trono D., Walker C.L.;
RT	"Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in
RT	kidney epithelial cell lines but not primary renal tumors.";

```

CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -!- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF064808; AAC23669.1; -.
CC EMBL; AF064808; AAC23670.1; -.
CC InterPro: IPR002110; -.
CC Pfam; PF00023; ank; 3.
CC PROSITE; PS50088; ANK_REPEAT; 1.
CC DR PROSITE; PS50297; ANK_REP_REGION; 1.
CC KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CC CHAIN 1 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
CC FT LONG ISOFORM.
CC FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
CC FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
CC FT SHORT ISOFORM.
CC FT FOR SHORT ISOFORM.
CC FT ANK 1.
CC FT REPEAT 45 74 ANK 1.
CC FT REPEAT 78 106 ANK 2.
CC FT REPEAT 111 140 ANK 3.
CC SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;

Query Match 51.0%; Score 408; DB 1; Length 171;
Best Local similarity 69.2%; Pred. No. 5.5e-31;
Matches 83; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 12 SADWLATAAARGVEEVRALEAVALPNAPNSYGRPRIOVMNMGSAARVAELLLHGAEPN 71
Db | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
46 SGKLTLEAARGTEVTELELGTNPNAVNRGRSAIQVMNMGNVRLAAAILLOYGAEPN 105
QY 72 CADPATLTREPVHDAAREGGFDLTLLVLRHAGARLDVRDAMGRLEPVDLAEEGLHRDVARYL 131
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
106 TPDPTLTLTLPVHDAAREGGFDLTLLVLRHAGARLDVRDAMGRLEPVDLAEEGHHLVVAYLR 165

RESULT 7
CDN7_HUMAN
ID CDN7_HUMAN STANDARD; PRT; 166 AA.
AC P5273; Q13102;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
GN CDKN2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96121373; PubMed=8575754;
RA Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J.,
RA Lahti J.M., Sherr C.J., Downing J.R.;
RT "Molecular cloning, expression pattern, and chromosomal localization
RT of human CDKN2D/INK4d, an inhibitor of cyclin D-dependent kinases.";
RL Genomics 23:633-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96362662; PubMed=8741839;

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RA	Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X., Zariwala M., Matera A.G., Xiong Y., "Isolation and characterization of p19INK4d, a p16-related inhibitor specific to CDK6 and CDK4.", Mol. Biol. Cell 7:57-70(1996).	QY	12	SADWLATAAARGVEEVREALL-EAVALPNAPNSYGRPRIOVMGMSARVAELLLHGAEP	70
RA		Db	8	AGDRLSAGAAAGDVOEVRRLLHRELVDALNREGKTKALQVMFGSTAIALLKOGASP	67
RT		QY	71	NCADPATLTRPVHDAAREGFLDTLVLHRRAGARLDVDAWGRPLPVDLAEBELGHRDVARYL	130
RL		Db	68	NVQDTSG-TSPVHDAARTGFLDTLVLEHGAADVNVDPDGTGALPHIAVOEGHTAVVSFL	126
RN	SEQUENCE FROM N.A.	QY	131	RAAAG---GTRGSNHARIDAAEGSPDIPD	156
RC	TISSUE=Thymus;	Db	127	AAESDLHRRDARGLTPLLELALQGAQDLVD	156
RX	MEDLINE=95257949; PubMed=7739548;				
RA	Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;				
RT	"Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to p16INK4.",				
RL	Mol. Cell. Biol. 15:2682-2688(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Newton Bishop J.A., Harland M., Bennett D.C., Bataille V., Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P., Bishop D.T.;				
RT	"Mutation testing in melanoma families: INK4A, CDK4 and INK4D.", Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.				
RL	[5]				
RN	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.				
RA	MEDLINE=98421670; PubMed=9751050;				
RX	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;				
RT	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor p16INK4a.",				
RL	Nature 395:237-243(1998).				
RN	[6]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RA	MEDLINE=98455510; PubMed=9782052;				
RX	Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Eng H.R.A., Holak T.A.;				
RT	"Structure of human cyclin-dependent kinase inhibitor p19(INK4d): comparison to known ankyrin-repeat-containing structures and implications for the dysfunction of tumor suppressor p16(INK4a).";				
RL	Structure 6:1279-1290(1998).				
CC	-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.				
CC	-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.				
CC	-!- SIMILARITY: CONTAINS 4 ANK REPEATS.				
CC	-----				
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CC	-----				
DR	EMBL; U49399; AAB03772.1; -				
DR	EMBL; U40343; AAB18139.1; -				
DR	EMBL; U20498; AAB85436.1; -				
DR	EMBL; AF061327; AAC27450.1; -				
DR	PDB; 1B18; 16-FEB-99.				
DR	PDB; 1BD8; 14-OCT-98.				
DR	MIN; 600927; -				
DR	InterPro: IPR002110; -				
DR	Pfam; PF00023; ank; 3.				
DR	PROSITE; PSS0088; ANK_REPEAT; 1.				
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.				
KW	Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure.				
FT	REPEAT 41 69				
FT	REPEAT 73 102				
FT	REPEAT 106 135				
FT	REPEAT 138 166				
FT	CONFLICT 159 159				
FT	SEQUENCE 166 AA; 17700 MW; 2FACDILICF56340DC CRC64;				
QY	32.48; Score 259; DB 1; Length 166;				
Best Local Similarity	44.08; Pred. No. 3e-17;				
Matches	66; Conservative 18; Mismatches 60; Indels 6; Gaps 3;				

Query Match	28.9%	Score 231.5	DB 1	Length 168
Best Local Similarity	40.3%	Pred. No. 1e-14		
Matches 56	Conservative 22	Mismatches 60	Indels 1	Gaps 1
QY	10	EPSADWLATAAAGRGVEEYRALLAEVALPNAIPNSYGRPQVMMGSGARVAELLLHGAE	69	
DB	3	EPWGNELASAAAGDLEQLTSLQNNVNVNAQNGFGRTALQVMKLGKNPETARRLLRGAN	62	
QY	70	PNCADPATLTPRVHDAAREGFLDTLVLLHRACGLDYRDAGRLPYVDLAEELGHRDVAR	129	
DB	63	PNLKD-GTGFVTHDRARAGFLDTVQLLEFQADVNIEDNEGLPHHLAAKEGHLPPVEF	121	
QY	130	LRAAAGGTGRGSHIARIDAA	148	
DB	122	LMKHATCNVGNHRNHKGDTA	140	
RESULT 10				
CDN6_HUMAN				
ID	CDN6_HUMAN	STANDARD	PRT	168 AA.
AC	P42773			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT			
DE	KINASE 4 INHIBITOR C) (P18-INK4C).			
GN	CDKN2C OR CDKN6.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID	9606;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=95095079; PubMed=8001816;			
RX	Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,			
RA	Matera G.A., Xiong Y.;			
RT	"Growth suppression by p18, a p18INK4/MTS1- and p18INK4B/MTS2-related			
RT	CDK6 inhibitor, correlates with wild-type pRB function.";			
RL	Genes Dev. 8:2939-2952(1994).			
RN	[2]			
RN	SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.			
RC	TTSUPE-Breast.			
RX	MEDLINE=98300299; PubMed=9636670;			
RA	Blaiss A., Labrie Y., Pouliot F., Lachance Y., Labrie C.;			
RT	"Structure of the gene encoding the human cyclin-dependent kinase			
RT	inhibitor p18 and mutational analysis in breast cancer.";			
RL	Biochem. Biophys. Res. Commun. 247:146-153(1998).			
RN	[3]			
RN	VARIANT BREAST CANCER PRO-72.			
RP	MEDLINE=96438606; PubMed=8840966;			
RX	Lapointe J., Lachance Y., Labrie Y., Labrie C.;			
RA	"A p18 mutant defective in CDK6 binding in human breast cancer			
RT	cells.";			
RL	Cancer Res. 56:4586-4589(1996).			
RN	[4]			
RN	X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).			
RP	MEDLINE=98100086; PubMed=9437433;			
RX	Venkataramani R., Swaminathan K., Marmorstein R.;			
RA	"Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides			
RT	insights into ankyrin-like repeat structure/function and			
RT	tumor-derived p18INK4 mutations.";			
RL	Nat. Struct. Biol. 5:74-81(1998).			
RN	[5]			
RN	STRUCTURE BY NMR.			
RP	MEDLINE=99175088; PubMed=10074345;			
RX	Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Maille P., Selby T.,			
RA	Tsai M.-D.;			
RT	"tumor suppressor INK4: determination of the solution structure of			
RT	p18INK4c and demonstration of the functional significance of loops in			
RL	p18INK4c and p16INK4A.";			
RL	Biochemistry 38:2930-2940(1999).			

FT	REPEAT	96	125	ANK 2.	DE
FT	REPEAT	129	158	ANK 3.	GN
FT	REPEAT	162	191	ANK 4.	OS
FT	REPEAT	193	220	ANK 5.	OC
FT	REPEAT	232	261	ANK 6.	OC
FT	REPEAT	265	294	ANK 7.	OX
FT	REPEAT	298	327	ANK 8.	RN
FT	REPEAT	331	360	ANK 9.	RP
FT	REPEAT	364	393	ANK 10.	RC
FT	REPEAT	397	426	ANK 11.	RX
FT	REPEAT	430	459	ANK 12.	RA
FT	REPEAT	463	492	ANK 13.	RT
FT	REPEAT	496	525	ANK 14.	RT
FT	REPEAT	529	558	ANK 15.	RL
FT	REPEAT	562	591	ANK 16.	CC
FT	REPEAT	595	624	ANK 17.	CC
FT	REPEAT	628	657	ANK 18.	CC
FT	REPEAT	661	690	ANK 19.	CC
FT	REPEAT	694	723	ANK 20.	CC
FT	REPEAT	727	756	ANK 21.	CC
FT	REPEAT	760	789	ANK 22.	CC
FT	REPEAT	793	822	ANK 23.	CC
FT	DOMAIN	1773	1950	REPEAT-RICH REGION.	CC
FT	REPEAT	1773	1784	REPEAT A.	CC
FT	REPEAT	1773	1784	REPEAT A.	CC
FT	REPEAT	1785	1796	REPEAT A.	CC
FT	REPEAT	1797	1808	REPEAT A.	CC
FT	REPEAT	1809	1820	REPEAT A.	CC
FT	REPEAT	1821	1832	REPEAT A.	CC
FT	REPEAT	1833	1844	REPEAT A.	CC
FT	REPEAT	1845	1856	REPEAT A.	CC
FT	REPEAT	1857	1867	REPEAT A.	CC
FT	REPEAT	1868	1879	REPEAT A.	CC
FT	REPEAT	1880	1891	REPEAT A.	CC
FT	REPEAT	1892	1902	REPEAT A.	CC
FT	REPEAT	1903	1914	REPEAT A.	CC
FT	REPEAT	1915	1926	REPEAT A.	CC
FT	REPEAT	1927	1938	REPEAT A.	CC
FT	REPEAT	1939	1950	REPEAT A.	CC
FT	DOMAIN	3536	3620	DEATH DOMAIN.	CC
FT	VARSPLIC	1039	1039	Q -> QFLGKLHPTAPPPLNAGESLSVRLQLGPPGTK (IN ISOFORM 2).	DR
FT	VARSPLIC	1444	3528	MISSING (IN ISOFORM 2 AND ISOFORM 3).	DR
FT	CONFLICT	475	476	GO -> PE (IN REF. 4).	DR
FT	CONFLICT	971	971	I -> S (IN REF. 2).	DR
FT	CONFLICT	3581	3582	QY -> HA (IN REF. 2).	DR
FT	CONFLICT	3586	3586	I -> Y (IN REF. 2).	DR
FT	SEQUENCE	3924 AA;	430337 MW;	52AC496C428E29D2 CRC64;	KW
Very Match					FT
Best Local Similarity					FT
Matches 48; Conservative 18; Mismatches 59; Indels 4; Gaps 3;					FT
QY	16	LATAAARGVEVRVALLLEAVLAPNPNSYGRRIQV-MMGSGARVAEALLLHGAEPNCAD 74			FT
Db	468	LHMAARAGQVVRVCLLRNGALVDARAREEQTPHLIASRLGKTEIVQLLQHMAHPDAA 527			FT
QY	75	PATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEELGHRVARYL--RA 132			FT
Db	528	TNGYT-PLHISAREQGVDSVLLLEAGAAHSLATKKGFTPLHVAAKYGLSDVAKILLQRR 586			FT
QY	133	AAAGTRGSN 141			FT
Db	587	AAADSAGN 595			FT
RESULT 12					
ANK1_MOUSE					
ID	ANK1_MOUSE	STANDARD;	PR1;	1862 AA.	
AC	002357;				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				

ANKYRIN 1 (ERYTHROCYTE ANKYRIN).	
ANK1 OR ANK-1.	
Mus musculus (Mouse).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI_TaxID=10090;	
[1]	
SEQUENCE FROM N.A.	
TISSUE=Erythrocyte;	
MEDLINE=92345717; PubMed=1386265;	
White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;	
"Murine erythrocyte ankyrin cDNA: highly conserved regions of the	
regulatory domain.";	
Mamm. Genome 3:281-285(1992).	
-!- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL	
ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO	
NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP95, AND TO THE	
CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.	
ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE	
CYTOSKELETAL DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;	
THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.	
-!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC	
PLASMA MEMBRANE.	
-!- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).	
-!- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).	
-!- SIMILARITY: CONTAINS 23 ANK REPEATS.	

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or send an email to license@sib-sib.ch).	

EMBL; M84756; AAA37236.1; -	
HSPP; Q00420; IAWC.	
MGD; MGI:88024; Ank1.	
InterPro; IPR000488; -	
InterPro; IPR000906; -	
InterPro; IPR002110; -	
Pfam; PF00791; ZU5; 1	
Pfam; PF00023; ank; 23	
Pfam; PF00531; death; 1	
PROSITE; PS50088; ANK_REPEAT; 20.	
PROSITE; PS50297; ANK_REPEAT_REGION; 1.	
PROSITE; PS50017; DEATH_DOMAIN; 1.	
Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.	
DOMAIN 1 827	
89 KDA DOMAIN (ANION EXCHANGE PROTEIN	
BINDING DOMAIN).	
DOMAIN 828 1386	
62 KDA DOMAIN (SPECTRIN BINDING	
DOMAIN).	
DOMAIN 1387 1862	
55 KDA REGULATORY DOMAIN (REGULATES	
THE BINDING OF ANKYRIN TO SPECTRIN	
AND THE BAND 3 PROTEIN).	
ANK 1.	
ANK 2.	
ANK 3.	
ANK 4.	
ANK 5.	
ANK 6.	
ANK 7.	
ANK 8.	
ANK 9.	
ANK 10.	
ANK 11.	
ANK 12.	
ANK 13.	
ANK 14.	
ANK 15.	
ANK 16.	
ANK 17.	
ANK 18.	


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FT VARIANT 462 462 /FTid-VAR_000595.
FT V -> I (IN HS).
FT /FTid-VAR_000596.
FT R -> H (IN BRUEGGEN).
FT /FTid-VAR_000597.
FT V -> A.
FT /FTid-VAR_000598.
FT D -> E.
FT /FTid-VAR_000599.
FT S -> T.
FT /FTid-VAR_000600.
FT E -> D.
FT /FTid-VAR_000601.
FT D -> N (IN DUESSELDORF).
FT /FTid-VAR_000602.
FT R -> D.
FT /FTid-VAR_000603.
FT CONFLICT 229 229 A -> S (IN REF. 2).
FT CONFLICT 1545 1545 V -> I (IN REF. 2).
FT SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFDICD428 CRC64;

Query Match 16.7%; Score 133.5; DB 1; Length 1880;
Best Local Similarity 35.4%; Pred. No. 0.00017;
Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;

QY 16 LATAAARGVEEVRLALAEVALPNAPNSYGRPIQV-MMGSGARVAELLLHGAEPNCAD 74
DB 506 LHIAAREGHVETLALLEKEASQACMTKKGFTPLHVAAYKGVKVAELLERDAHPNAAG 565
QY 75 PATITRVHDAAREGFLDTL-VVLHAGARLDVRDAW-GELPVDLAEELGHRDVARYL-- 130
DB 566 KNGLT-PLHVAVHHNNLDIVKLLPRGGS--PHSPAWNGYTPPLHIAAKQNOVEVARSLQ 622
QY 131 ---RAAAGTGRGNHARIDAAEGPSDI 154
DB 623 YGGSANAEVQGVTPPLHAAQEGHAEM 649

RESULT 14
DAPK_HUMAN STANDARD; PRT; 1431 AA.
AC P53355;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
GN DAPK1 OR DAPK.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95129831; PubMed=7828849;
RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT "Identification of a novel serine/threonine kinase and a novel 15-kD
RT protein as potential mediators of the gamma interferon-induced cell
RT death.";
RL Genes Dev. 9:15-30(1995).
RN [2]
RP REVISIONS TO 164-171.
RA Feinstein E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC DEATH.
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL; X76104; CAA53712.1; -.
DR HSP; Q63450; IA06.
DR MIM; 600831; -.
DR InterPro; IPR000488; -.
DR InterPro; IPR000719; -.
DR InterPro; IPR002110; -.
DR InterPro; IPR002290; -.
DR Pfam; PF00023; ank; 8.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS50088; ANK_REPEAT; 6.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50107; DEATH_DOMAIN; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
DR Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
KW DOMAIN 13 266 PROTEIN KINASE.
FT DOMAIN 267 334 CALMODULIN-BINDING.
FT REPEAT 378 407 ANK 1.
FT REPEAT 411 440 ANK 2.
FT REPEAT 444 473 ANK 3.
FT REPEAT 478 507 ANK 4.
FT REPEAT 511 540 ANK 5.
FT REPEAT 544 573 ANK 6.
FT REPEAT 577 606 ANK 7.
FT REPEAT 610 639 ANK 8.
FT REPEAT 676 705 ANK 9.
FT REPEAT 1163 1197 ANK 10.
FT DOMAIN 1313 1397 DEATH.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
SQ SEQUENCE 1431 AA; 160017 MW; 9EB84811004A155B CRC64;

Query Match 16.3%; Score 130.5; DB 1; Length 1431;
Best Local Similarity 29.18; Pred. No. 0.00024;
Matches 44; Conservative 14; Mismatches 54; Indels 39; Gaps 4;

QY 16 LATAAARGVEEVRLALAEVALPNAPNSYGRPIQVMMGSGAR----VAEILLHGAEPN 71
DB 483 LHCAAWHGYSYVAKALCEAGCNVNIKNEGETP---LLTASARGYHDIVECLAERGADLN 539
QY 72 CADP-----ATL-----TRPVDAAREGFLDTLVVLR 99
DB 540 ACDKDGHTALHLAVRRCOMEVIKTLISQGCYVDYQDRHGNTPLHVACKDGNMPTVVALCE 599
QY 100 AGARLDVRDAMGRPLVDLAEELGHRDVARYL 130
DB 600 ANCNLDISNKYGRTPPLHAAANNGLDVVRYL 630

RESULT 15
NTC4_MOUSE STANDARD; PRT; 1964 AA.
AC P31695; 062389;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING
DE PROTEIN INT-3).
GN NOTCH4 OR INT3 OR INT-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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FT DISULFID 595 610 BY SIMILARITY.
FT DISULFID 612 621 BY SIMILARITY.
FT DISULFID 626 637 BY SIMILARITY.
FT DISULFID 631 646 BY SIMILARITY.
FT DISULFID 648 655 BY SIMILARITY.
FT DISULFID 662 669 BY SIMILARITY.
FT DISULFID 664 674 BY SIMILARITY.
FT DISULFID 676 685 BY SIMILARITY.
FT DISULFID 692 703 BY SIMILARITY.
FT DISULFID 697 712 BY SIMILARITY.
FT DISULFID 714 723 BY SIMILARITY.
FT DISULFID 730 741 BY SIMILARITY.
FT DISULFID 735 750 BY SIMILARITY.
FT DISULFID 752 761 BY SIMILARITY.
FT DISULFID 768 779 BY SIMILARITY.
FT DISULFID 773 788 BY SIMILARITY.
FT DISULFID 790 799 BY SIMILARITY.
FT DISULFID 807 818 BY SIMILARITY.
FT DISULFID 812 827 BY SIMILARITY.
FT DISULFID 829 838 BY SIMILARITY.
FT DISULFID 845 856 BY SIMILARITY.
FT DISULFID 850 865 BY SIMILARITY.
FT DISULFID 867 876 BY SIMILARITY.
FT DISULFID 882 903 BY SIMILARITY.
FT DISULFID 897 912 BY SIMILARITY.
FT DISULFID 914 923 BY SIMILARITY.
FT DISULFID 930 941 BY SIMILARITY.
FT DISULFID 935 950 BY SIMILARITY.
FT DISULFID 952 961 BY SIMILARITY.
FT DISULFID 968 979 BY SIMILARITY.
FT DISULFID 973 988 BY SIMILARITY.
FT DISULFID 990 999 BY SIMILARITY.
FT DISULFID 1006 1019 BY SIMILARITY.
FT DISULFID 1011 1028 BY SIMILARITY.
FT DISULFID 1030 1039 BY SIMILARITY.
FT DISULFID 1046 1057 BY SIMILARITY.
FT DISULFID 1051 1069 BY SIMILARITY.
FT DISULFID 1071 1080 BY SIMILARITY.
FT DISULFID 1087 1098 BY SIMILARITY.
FT DISULFID 1092 1110 BY SIMILARITY.
FT DISULFID 1112 1121 BY SIMILARITY.
FT DISULFID 1130 1142 BY SIMILARITY.
FT DISULFID 1136 1155 BY SIMILARITY.
FT DISULFID 1157 1166 BY SIMILARITY.

Query Match 15.6%; Score 125; DB 1; Length 1964;
Best Local Similarity 25.5%; Pred. No. 0.0011;
Matches 52; Conservative 16; Mismatches 66; Indels 70; Gaps 5;

16 LATAAARGVEEVALLLEVALPNAPNSYGRPTQVMGMSAR-VAELLL----- 64
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1633 LHAAARFSPRTAARRLLEAGANPNQPDAGRTPLHTAADAAREVCQLLLASRQTSVDAR 1692
Qy 65 -----LH-----G 67
| |
Db 1693 TEDGTTPLMLAARLAVEDLVEELIAARADYGARDKRGKTALHMAAAVNNARAARSLQAG 1752
Qy 68 AEPNCADPATLTPRVHDAAREGFLDTLVLLHRAGARLDVRDAGRLPVDLAEELGHRDVA 127
| : : | : : | : : | : : | : : | : : | : : | : : | : :
Db 1753 ADKDAQSREGT-PLFLAAREGAVEVAQLLLELGARGLRDQAGLAPGVARORSHWDL 1811
Qy 128 RYLRAAAGGTRGSN-HARIDAAEG 150
| | | | |
Db 1812 TLLEGAGTTQEARAHARTTPGGG 1835
```


Query Match	59.2%;	Score 474;	DB 11;	Length 168;
Best Local Similarity	63.2%;	Pred. NO. 1.2e-33;		
Matches 98;	Conservative 17;	Mismatches 32;	Indels 8;	Gaps 27

Query Match 59.2%; Score 474; DB 11; Length 168;
Best Local Similarity 63.2%; Pred. No. 1.2e-33;
Matches 98; Conservative 17; Mismatches 32; Indels

QY 9 MEPSADNWTATAAAGRVEEVETALLLEAVALPNAPNSYGRRPQTQVMMGSGARVAELL

RESULT 6

RESULT	6
09XS51	
ID	Q9XS51 PRELIMINARY; PRT; 102 AA.
AC	Q9XS51;
DT	01-NOV-1999 (IREMBLrel. 12, Created)
DT	01-NOV-1999 (IREMBLrel. 12, Last sequence update)
DT	01-MAR-2001 (IREMBLrel. 15, Last annotation update)
DE	P16/CDKMZA/WTS1 (FRAGMENT);
OS	Felis silvestris catus (Cat).
OC	Eukaryota; Metazoa; Chordata;
OX	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
NCBI_TaxID=9685;	[1]
RN	SEQUENCE FROM N.A.

```

EL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -.
DR HSP; PA2771; IBI7.
DR InterPro: IPR002110; -.
DR Pfam: PF00023; ank; 3.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT non_ter
FT non_ter 1
FT non_ter 102 102
FT non_ter 102 102
FT non_ter 102 AA; 10824 MW; 263999FF21359F35D CRC64;
SQ

```

Query Match 56.1%; Score 449; DB 6; Length 102;


```
SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;

Query Match 50.6%; Score 405; DB 11; Length 86;
Best Local Similarity 91.8%; Pred. No. 5e-28; 3; Indels 0; Gaps 0;
Matches 78; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 51 VMWMSARVAELLLHGAEPNCADPATLTLPVHDAAREGFDTLVVLRHAGARLDVRDAW 110
   1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 VMWMSARVAELLLHGAEPNCADPATLTLPVHDAAREGFDTLVVLRHAGARLDVRDAW 60
   1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||

QY 111 GRLPVDLAELGHRDVARYLRAAG 135
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GRLPVDLAELGHRDVARYLHAASG 85
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
Q921C2 PRELIMINARY; PRT; 113 AA.
Q921C2;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P16.
OC Mus spretus (Western wild mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/ET;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RT Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79634; AAD00236.1; -.
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 2.
DR SMART; SM00248; ANK; 1.
DR Kinase; Cyclin.
KW NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12073 MW; C3BFE8325DB2D79E CRC64;

Query Match 41.8%; Score 334; DB 11; Length 113;
Best Local Similarity 61.1%; Pred. No. 9.1e-22;
Matches 69; Conservative 12; Mismatches 24; Indels 8; Gaps 2;

QY 51 VMWMSARVAELLLHGAEPNCADPATLTLPVHDAAREGFDTLVVLRHAGARLDVRDAW 110
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 1 VMWMSARVAELLLHGAEPNCADPATLTLPVHDAAREGFDTLVVLRHAGARLDVRDAW 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||

QY 111 GRLPVDLAELGHRDVARYLRAA-----AGGT--RGSNHARIDAAGPSDIP 155
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 GRLPDLAQERGHQDIVVRLRSAGCSLCTAGNVAQTGDHGSFSSSTP 113
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

RESULT 15
Q9QWH5 PRELIMINARY; PRT; 113 AA.
Q9QWH5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P16.
OS Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUS MUSCULUS;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RT Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79633; AAD00230.1; -.
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 2.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase; Cyclin.
FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12170 MW; 5D4DE8325D06638B CRC64;

Query Match 41.4%; Score 331; DB 11; Length 113;
Best Local Similarity 60.2%; Pred. No. 1.7e-21;
Matches 68; Conservative 13; Mismatches 24; Indels 8; Gaps 2;

QY 51 VMWMSARVAELLLHGAEPNCADPATLTLPVHDAAREGFDTLVVLRHAGARLDVRDAW 110
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 1 VMWMSARVAELLLHGAEPNCADPATLTLPVHDAAREGFDTLVVLRHAGARLDVRDAW 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||

QY 111 GRLPVDLAELGHRDVARYLRAA-----AGGT--RGSNHARIDAAGPSDIP 155
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 GRLPDLAQERGHQDIVVRLRSAGCSLCTAGNVAQTGDHGSFSSSTP 113
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

Search completed: October 31, 2001, 07:13:46
Job time: 538 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:02:33 ; Search time 51.96 Seconds
(without alignments)
182.012 Million cell updates/sec

Title: US-09-016-869A-2
Perfect score: 800
Sequence: 1 MDPAGSMPEPSDLATAA.....TRGSHARIDAEGPSDIPD 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
1 number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
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12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
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14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
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16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	800	100.0	156	16 AAR85116	Cell-cycle regulat
2	800	100.0	156	20 AAY24741	Human INK-4 protei
3	800	100.0	156	21 AAY88354	Human cell cycle r
4	789	98.6	156	18 AAW10627	Tumour suppressor
5	789	98.6	156	18 AAW19251	Human multiple tum
6	789	98.6	156	19 AAW74549	Amino acid sequenc
7	789	98.6	156	19 AAW40524	Human MTS1 protein
8	789	98.6	156	20 AAW80524	A human multiple t
9	789	98.6	156	21 AAB15498	Human MTS1 protein
10	789	98.6	156	21 AAY97524	Human p16 protein
11	789	98.6	156	21 AAY96053	Human cyclin depen

12	789	98.6	156	21	AAY96067	Human cyclin depen
13	789	98.6	156	21	AAY92921	Human multiple tum
14	789	98.6	156	21	AAY91102	Human multiple tum
15	789	98.6	156	21	AAY59415	Human MTS1 protein
16	789	98.6	156	21	AAY54902	Human multiple tum
17	789	98.6	156	22	AAB67334	Protein encoded by
18	789	98.6	156	22	AAB36890	Human Multiple Tum
19	788	98.5	228	21	AAY97522	Human W9 protein s
20	788	98.5	228	21	AAY96051	Antiproliferative
21	788	98.5	228	21	AAY96078	Angiogenesis inhib
22	788	98.5	237	20	AAW95105	Truncated p27/p16
23	788	98.5	237	21	AAY97534	Human W9 protein s
24	788	98.5	237	21	AAY96049	Antiproliferative
25	788	98.5	237	21	AAY96076	Angiogenesis inhib
26	788	98.5	252	20	AAW95106	Truncated p27/p16
27	788	98.5	252	21	AAY97535	Human W10 protein
28	788	98.5	252	21	AAY96050	Antiproliferative
29	788	98.5	323	21	AAY96079	Angiogenesis inhib
30	788	98.5	323	21	AAY96079	Secretable angio
31	788	98.5	334	20	AAW95103	Truncated p27/p16
32	788	98.5	334	21	AAY97532	Human W8 protein s
33	788	98.5	334	21	AAY96047	Antiproliferative
34	788	98.5	334	21	AAY96074	Angiogenesis inhib
35	788	98.5	365	18	AAW23536	CDK inhibitory fus
36	788	98.5	365	20	AAW95107	Human p16p27 fusio
37	788	98.5	365	20	AAW95096	Human p16p27 fusio
38	788	98.5	365	21	AAY97527	Human W4 protein s
39	788	98.5	365	21	AAY97529	Human W6 protein s
40	788	98.5	365	21	AAY96042	Antiproliferative
41	788	98.5	365	21	AAY96044	Antiproliferative
42	788	98.5	365	21	AAY96069	Angiogenesis inhib
43	788	98.5	365	21	AAY96071	Angiogenesis inhib
44	788	98.5	380	18	AAW23535	CDK inhibitory fus
45	788	98.5	380	20	AAW95095	Human p16(GS)p27 f

ALIGNMENTS

RESULT 1	
AAR85116	
ID	AAR85116 standard; Protein; 156 AA.
XX	
AC	AAR85116;
XX	
DT	01-MAR-1996 (first entry)
XX	
DE	Cell-cycle regulatory protein p16.
XX	
KW	Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
KW	CCR; cancer; cell proliferation.
XX	
OS	Homo sapiens.
XX	
XX	
PN	WO9528483-A1.
PD	26-OCT-1995.
XX	
PF	14-APR-1995; 95WO-US04636.
XX	
PR	29-NOV-1994; 94US-0346147.
PR	14-APR-1994; 94US-0227371.
PR	25-MAY-1994; 94US-0248812.
PR	14-SEP-1994; 94US-0306511.
XX	
PA	(COLD-) COLD SPRING HARBOR LAB.
XX	
PI	Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
XX	
DR	WPI; 1995-373798/48.
DR	N-PSDB; AAT02962.
XX	
PT	New cell cycle regulating proteins bind to cyclin dependent kinase -

PT and related nucleic acids, antibodies etc., used in diagnosis and
 PT therapy of abnormal cell proliferation, degeneration etc.

PS Claim 1; Page 76-77; 109pp; English.

XX The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was
 CC obtd. by expression of a cDNA clone (AA02962) isolated in a 2-hybrid
 CC screening assay. CCR p16 specifically inhibits the activity of
 CC cyclin-dependent kinases during various stages of the cell cycle,
 CC and can be used in the treatment and diagnosis of proliferative
 CC disorders.

XX Sequence 156 AA;

Query Match 100.0%; Score 800; DB 16; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.6e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MDPAGSSMEPSADWLATAAARGVEVRALLEAVALPNAPNSYGRRPQVMMMGSAARVA 60
 1 mdpagssmepsadwlataaargveevrallleavlpnapnsygrripqvmmgsgarva 60
 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEE 120
 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlrhagarldvrdawgrlpvdlae 120
 121 LGHRDVARYLRAAAGTGRGSHARIDAAGPSDIPD 156
 121 lghrdvarylraaagtrgrsharidaaegpsdipd 156

RESULT 2

AAAY24741
 ID AAY24741 standard; Protein; 156 AA.

XX AC AAY24741;

XX DT 23-AUG-1999 (first entry)

XX DE Human INK-4 protein p16.

XX INK-4; p16; p15; p18; CDK4; cell cycle regulatory protein;
 KW transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.

XX OS Homo sapiens.

XX US5919997-A.

XX 06-JUL-1999.

XX 04-APR-1996; 96US-0627610.

XX 04-APR-1996; 96US-0627610.

XX 18-NOV-1993; 93US-0154915.

XX 14-APR-1994; 94US-0227371.

XX 25-MAY-1994; 94US-0248812.

XX 14-SEP-1994; 94US-0306511.

XX 29-NOV-1994; 94US-0346147.

XX 30-JUN-1995; 95US-0497214.

XX 02-JAN-1996; 96US-0581918.

XX (COLD-) COLD SPRING HARBOR LAB.

XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.

XX Beach DH, DePinho RA, Serrano M;

XX WPI; 1999-394656/33.

XX N-PSDB; AAX80472.

XX Transgenic mice with modified cell-cycle regulation

XX Disclosure; Column 45-46; 35pp; English.

XX The present invention describes a transgenic mouse having germline and
 CC somatic cells which comprise an incorporated transgene that disrupts and
 CC inhibits the p16-INK4-a gene leading to tumour susceptibility. Also
 CC described is a method of making a mouse and mouse embryonic stem cells a
 CC functionally disrupted p16-INK4-a gene which comprises transferring a
 CC transgene construct into embryonic stem cells of a mouse and
 CC transferring these into a mouse blastocyst and implanting the resulting
 CC chimeric blastocyst into a female mouse selecting offspring having an
 CC endogenous p16-INK4-a gene allele. The transgenic mouse is useful for
 CC evaluating the carcinogenic potential or the anti-proliferative activity
 CC of a test compound. The present sequence represents the human INK4
 CC protein p16 given in the present invention.

XX Sequence 156 AA;

Query Match 100.0%; Score 800; DB 20; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.6e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MDPAGSSMEPSADWLATAAARGVEVRALLEAVALPNAPNSYGRRPQVMMMGSAARVA 60
 Db 1 mdpagssmepsadwlataaargveevrallleavlpnapnsygrripqvmmgsgarva 60
 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEE 120
 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlrhagarldvrdawgrlpvdlae 120
 121 LGHRDVARYLRAAAGTGRGSHARIDAAGPSDIPD 156
 121 lghrdvarylraaagtrgrsharidaaegpsdipd 156

RESULT 3

AAAY88354
 ID AAY88354 standard; Protein; 156 AA.

XX AC AAY88354;

XX DT 14-JUL-2000 (first entry)

XX DE Human cell cycle regulatory protein p16 amino acid sequence.

XX Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection;
 KW cell proliferation; differentiation; neoplasia; cancer; cell growth;
 KW cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.

XX OS Homo sapiens.

XX PN US6043030-A.

XX PD 28-MAR-2000.

XX 02-JAN-1996; 96US-0581918.

XX 17-DEC-1992; 92US-0991997.

XX 18-NOV-1993; 93US-0154915.

XX 14-APR-1994; 94US-0227371.

XX 25-MAY-1994; 94US-0248812.

XX 14-SEP-1994; 94US-0306511.

XX 29-NOV-1994; 94US-0346147.

XX 30-JUN-1995; 95US-0497214.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Beach DH, Demetrick DJ, Serrano M, Hannon GJ;

XX WPI; 2000-270336/23.

XX N-PSDB; AAA13096.

XX Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory
 PT protein) in a diagnostic assay for identifying a cell at risk for a

PT disorder characterized by unwanted cell proliferation or
XX differentiation -
PS Claim 14; Column 57-58; 61pp; English.
XX
CC This sequence represents the human cell cycle regulatory protein (CCR)
CC p16 amino acid sequence. The p16 gene is located on chromosome 9p21-22.
CC The invention relates to a diagnostic assay which comprises detecting a
CC mutation in the p16 gene, which is used to identify a cell or cells at
CC risk of developing a disorder characterized by unwanted cell
CC proliferation or differentiation. p16 is a cyclin-dependent kinase
CC (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle
CC progression and ultimately cell growth. The assay can be used for
CC identifying a cell or cells at risk for a disorder (neoplasia)
CC characterized by unwanted cell proliferation or differentiation. The
CC method is used for detecting mutations in either a CCR gene or CDK gene
CC which alter complex formation between these two proteins. The method is
CC also used for detecting mutations in other cellular proteins which
CC disrupt protein interactions such as mutations which disrupt binding of
CC the p53 protein with other cellular proteins, e.g. Wilms' tumour
CC suppressor protein Wt1. They can also be used to detect mutations in
CC pairs of signal transduction proteins such as ras protein or other
CC cellular proteins which interact with ras, e.g. ras GTPase activating
CC proteins (GAPs). The method is convenient for detecting mutants of CCR
CC genes encoding proteins which are unable to physically interact with a
CC CDK bait protein.
XX
SQ Sequence 156 AA;

Query Match 100.0%; Score 800; DB 21; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.6e-86;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPAAAGSMPEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRPIQVMMGMSARVA 60
DB 1 mdpaaagsmepsadwataaargveevrallleavallpnapsygrripqvmummsarva 60
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
DB 61 ellllhgaepncadpatltrpvhdaaregfldtlvvlhragardlvdrdawgrlpvdlae 120
QY 121 LGRDVARVYLRRAAGGTRGSHARIDAAEGPSDIPD 156
DB 121 lgrdvarylraaaggtgrgsharidaaegpsdipd 156

RESULT 4
AAW10627
XX AAW10627 standard; Protein; 156 AA.
XX
XX AAW10627;
XX
XX 28-OCT-1997 (first entry)
XX
XX Tumour suppressor p16.
XX
XX Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;
XX cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
XX anti-angiogenic activity; hyperproliferative disorder.
XX
XX Homo sapiens.
XX
XX WO9703635-A2.
XX
XX 06-FEB-1997 96WO-US11787.
XX
XX 17-JUL-1996;
XX
XX 17-JUL-1995 95US-0502881.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX

PI Jin X, Roth J;
XX WPI; 1997-132336/12.
DR N-PSDB; AAT60951.
XX
XX Expression construct contg. DNA for tumour suppressor p16 - to
XX restore p16 activity to transformed cells, useful for treating lung
XX or bladder cancer or melanoma
XX
XX Disclosure; Fig 1b; 92pp; English.
XX
XX This sequence represents the tumour suppressor p16. The DNA encoding
XX this sequence is joined to a promoter functional in eukaryotic cells and
XX used in the expression construct of the invention. p16 is an inhibitory
XX subunit, which is involved in the control of cyclin-dependent kinase 4
XX activity, and functions as a tumour suppressor. By detecting this
XX sequence or the DNA encoding it, cancer cells can be detected. When the
XX nucleic acid molecule is in the sense orientation, the expression
XX construct can be used to restore p16 function in a cell, particularly by
XX reversing the transformed phenotype in tumours, especially lung or
XX bladder cancer or melanoma. It may also have anti-angiogenic activity,
XX and inhibit hyperproliferative disorders, e.g. restenosis. When the
XX nucleic acid molecule is inserted in the antisense orientation, the
XX expression construct inhibits p16 function. Reduced or increased levels
XX of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by
XX Northern or Northern blot, antibody immunoblot, fluorescent cell sorting
XX or immunoassay.
XX
SQ Sequence 156 AA;

Query Match 98.6%; Score 789; DB 18; Length 156;
Best Local Similarity 98.7%; Pred. No. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDPAAAGSMPEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRPIQVMMGMSARVA 60
DB 1 mdpaaagsmepsadwataaargveevrallleavallpnapsygrripqvmummsarva 60
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
DB 61 ellllhgaepncadpatltrpvhdaaregfldtlvvlhragardlvdrdawgrlpvdlae 120
QY 121 LGRDVARVYLRRAAGGTRGSHARIDAAEGPSDIPD 156
DB 121 lgrdvarylraaaggtgrgsharidaaegpsdipd 156

RESULT 5
AAW19251
XX AAW19251 standard; Protein; 156 AA.
XX
XX AAW19251;
XX
XX 10-SEP-1997 (first entry)
XX
XX Human multiple tumour suppressor 1 gene product.
XX
XX Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
XX
XX Homo sapiens.
XX
XX US5624819-A.
XX
XX 29-APR-1997.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 07-JUN-1995; 95US-0474177.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 18-MAR-1994; 94US-0215086.
XX
XX 18-MAR-1994; 94US-0215087.
XX
XX 14-APR-1994; 94US-0227369.
XX

PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03537.
XX (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX Cannon-Albright LA, Kamb A, Skolnick MH;
PI WPI; 1997-258217/23.
DR N-PSDB; AAT72311.
XX Human mutant multiple tumour suppressor gene sequences - for
PT production of recombinant mutant polypeptide(s)
XX Claim 1; Columns 61-64; 72pp; English.
PS The present sequence the human multiple tumour suppressor 1
CC (MTS1) gene product, useful in cancer diagnosis.
XX Sequence 156 AA;
Query Match 98.6%; Score 789; DB 18; Length 156;
Best Local Similarity 98.7%; Pred. NO. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPVQVMMGSAARVA 60
Db 1 mepaagssmepsadwlataaaargveevrllleagalpnapnsygrripqvmmggsarva 60
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
Db 61 ellllhgaepncadpatltrpvhdaaregfdtlvvlrharaldvdrdawgrlpvdlae 120
QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
Db 121 lghrdvarylraaagtgtrgsnharidaaegpsdipd 156
RESULT 6
AAW74549
ID AAW74549 standard; Protein; 156 AA.
XX AC AAW74549;
XX DT 04-DEC-1998 (first entry)
XX Amino acid sequence of multiple tumour suppressor 1.
XX Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy.
XX Homo sapiens.
XX US5801236-A.
XX PD 01-SEP-1998.
XX PF 07-JUN-1995; 95US-0480810.
XX PR 07-JUN-1995; 95US-0480810.
XX PR 18-MAR-1994; 94US-0214582.
XX PR 18-MAR-1994; 94US-0215086.
XX PR 18-MAR-1994; 94US-0215087.
XX PR 14-APR-1994; 94US-0227369.
XX PR 01-JUN-1994; 94US-0251938.
XX PR 17-MAR-1995; 95WO-US03316.
XX (MYRI-) MYRIAD GENETICS INC.
XX Kamb A;
XX WPI; 1998-494842/42.
XX

DR N-PSDB; AAV53819.
XX Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
XX Disclosure; Column 63-64; 73pp; English.
XX This is the amino acid sequence of the multiple tumour suppressor 1
CC (MTS-1) protein, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
XX Sequence 156 AA;
SQ
Query Match 98.6%; Score 789; DB 19; Length 156;
Best Local Similarity 98.7%; Pred. NO. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPVQVMMGSAARVA 60
Db 1 mepaagssmepsadwlataaaargveevrllleagalpnapnsygrripqvmmggsarva 60
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
Db 61 ellllhgaepncadpatltrpvhdaaregfdtlvvlrharaldvdrdawgrlpvdlae 120
QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
Db 121 lghrdvarylraaagtgtrgsnharidaaegpsdipd 156
RESULT 7
AAW40524
ID AAW40524 standard; Protein; 156 AA.
XX AC AAW40524;
XX DT 15-JUL-1998 (first entry)
XX Human Mts1 protein.
XX MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition.
XX Homo sapiens.
XX US5739027-A.
XX PN 14-APR-1998.
XX PD 07-JUN-1995; 95US-0487033.
XX PF 07-JUN-1995; 95US-0487033.
XX PR 18-MAR-1994; 94US-0214582.
XX PR 18-MAR-1994; 94US-0215086.
XX PR 18-MAR-1994; 94US-0215087.
XX PR 14-APR-1994; 94US-0227369.
XX PR 01-JUN-1994; 94US-0251938.
XX PR 17-MAR-1995; 95WO-US03316.
XX (MYRI-) MYRIAD GENETICS INC.
XX PA
XX

PI Kamb A;
XX WPI; 1998-250421/22.
DR N-PSDB; AAV11238.
XX
XX DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
XX
XX Disclosure; Column 63-64; 72pp; English.
XX
XX This sequence represents a human multiple tumour suppression protein,
CC MTS1. The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.
XX
XX Sequence 156 AA;

Query Match 98.6%; Score 789; DB 19; Length 156;
Best Local Similarity 98.7%; Pred. No. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLAEVALPNAPNSYGRRPQVMMGSGARVA 60
Db 1 mepaagssmepsadwlataaargveevrllaeagalpnapnsygrripqvmmgsgarva 60

QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEE 120
Db 61 e111llhgaepncadpatitrvphdaaregfdltlvvlhragardvrdawgripvdlae 120

QY 121 LGRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
Db 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156

RESULT 8
AAW80524
ID AAW80524 standard; Protein; 156 AA.
XX
XX AAW80524;
XX
XX 03-FEB-1999 (first entry)
XX
XX A human multiple tumour suppressor 1 (MTS1) protein.
XX
XX Human; multiple tumour suppressor 1 gene; MTS1; cancer.
XX
XX Homo sapiens.
XX
XX US5843756-A.
XX
XX 01-DEC-1998.
XX
XX 28-JUL-1995; 95WO-0508735.
XX
XX 28-JUL-1995; 95US-0508735.
XX
XX 07-JUN-1995; 95US-0487033.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Jiang P, Kamb A, Stone S;
XX
XX WPI; 1999-044585/04.
DR N-PSDB; AAV70583.
XX
XX Mouse multiple tumour suppressor gene segment - useful for primer
PT design
XX
XX Disclosure; Columns 65-66; 80pp; English.

XX The present sequence represents a human multiple tumour suppressor 1
CC (MTS1) protein. The sequence is homologous to the corresponding
CC murine gene. Primers designed from the gene can be used to design
CC primers to detect abnormalities i.e. polymorphisms which may
CC predispose towards malignancies such as melanoma, leukaemia,
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
XX
XX Sequence 156 AA;

Query Match 98.6%; Score 789; DB 20; Length 156;
Best Local Similarity 98.7%; Pred. No. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLAEVALPNAPNSYGRRPQVMMGSGARVA 60
Db 1 mepaagssmepsadwlataaargveevrllaeagalpnapnsygrripqvmmgsgarva 60

QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEE 120
Db 61 e111llhgaepncadpatitrvphdaaregfdltlvvlhragardvrdawgripvdlae 120

QY 121 LGRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156
Db 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156

RESULT 9
AAB15498
ID AAB15498 standard; Protein; 156 AA.
XX
XX AAB15498;
XX
XX 14-FEB-2001 (first entry)
XX
XX Human MTS1 protein.
XX
XX Cytostatic; human; multiple tumour suppressor 1; MTS1; diagnostic;
KW cancer; gene therapy; protein replacement therapy.
XX
XX Homo sapiens.
XX
XX US6090578-A.
XX
XX 18-JUL-2000.
XX
XX 08-DEC-1997; 97US-0986515.
XX
XX 07-JUN-1995; 95US-0480810.
XX
XX 18-MAR-1994; 94US-0214582.
XX
XX 18-MAR-1994; 94US-0215086.
XX
XX 18-MAR-1994; 94US-0215087.
XX
XX 14-APR-1994; 94US-0227369.
XX
XX 01-JUN-1994; 94US-0251938.
XX
XX 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX
XX WPI; 2000-514036/46.
DR N-PSDB; AAA95633.
XX
XX Novel protein composition useful in protein replacement therapy for
PT diagnosing and treating cancer comprises a specific weight percent of
PT human multiple tumour suppressor 1 polypeptide -
XX
XX Claim 4; Column 63-64; 72pp; English.
XX
XX This sequence represents the human multiple tumour suppressor 1 (MTS1)
CC amino acid sequence. The protein has a cytostatic activity and is used in

CC protein replacement therapy. WTS1 is useful in diagnosing human cancers
CC such as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma,
CC glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma,
CC cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of
CC pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary,
CC uterus, testis, kidney, colon and rectum. The WTS1 gene and protein is
CC useful in gene therapy, protein replacement therapy and protein mimetic
CC studies.

XX Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;
Best Local Similarity 98.7%; Pred. No. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPRPQVMMGMSARVA 60

Db 1 mepaagssmepsadwlataaargveevrallleagalpnapnsygrprpqvmmgmsarva 60

61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120

Db 61 ellllhgaepncadpatltrpvhdaaregfltdlvvlhragardlvrddawgripvdlae 120

QY 121 LGRDVARYLRAAAGGTRGSHARIDAEGPSDIPD 156

Db 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156

RESULT 10

AA97524

ID AA97524 standard; Protein; 156 AA.

XX AC AA97524;

XX 15-JAN-2001 (first entry)

XX Human p16 protein sequence.

XX Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy;

XX adenovirus E4 protein; neoplasia; p16 protein.

XX Homo sapiens.

XX WO200052184-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US05350.

XX 01-MAR-1999; 99US-0122974.

XX 08-APR-1999; 99US-0128271.

XX 09-APR-1999; 99US-0128515.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;

XX WPI; 2000-587315/55.

XX N-PSDB; AAA90921.

XX Protein and nucleic acid compositions for preventing and treating

XX neoplasias (particularly cancer), comprises a novel chimeric cyclin

XX dependent kinase inhibitor and adenovirus E4 protein -

XX Example 1; Page 123; 126pp; English.

XX This sequence represents the human p16 protein.

XX The invention relates to a protein composition comprising a novel

XX purified chimeric cyclin dependent kinase inhibitor (CDKi) and a

XX purified adenovirus E4 protein. The compositions comprising the protein,

XX or the DNA encoding it are useful for treating neoplasias in animals. The

CC compositions also find use in assays to eliminate a specific
CC sub-population of cultured cells, to determine the susceptibility of
CC neoplastic cells to treatment with the compositions and also in assays to
CC synchronise cell growth in cultured cells.

XX Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;
Best Local Similarity 98.7%; Pred. No. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPRPQVMMGMSARVA 60

Db 1 mepaagssmepsadwlataaargveevrallleagalpnapnsygrprpqvmmgmsarva 60

QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120

Db 61 ellllhgaepncadpatltrpvhdaaregfltdlvvlhragardlvrddawgripvdlae 120

QY 121 LGRDVARYLRAAAGGTRGSHARIDAEGPSDIPD 156

Db 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156

RESULT 11

AA96053

ID AA96053 standard; Protein; 156 AA.

XX AC AA96053;

XX 05-DEC-2000 (first entry)

XX Human cyclin dependent kinase inhibitor p16.

XX Cyclin dependent kinase inhibitor; CDKi; INK4; human; p16;

XX smooth muscle cell; restenosis; vasotropic; antiproliferative;

XX gene therapy.

XX Homo sapiens.

XX WO200052159-A1.

XX 08-SEP-2000.

XX 28-FEB-2000; 2000WO-US04971.

XX 01-MAR-1999; 99US-0122974.

XX 05-NOV-1999; 99US-0163682.

XX 09-DEC-1999; 99US-0457568.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX McArthur J, Gyuris J, Finer M;

XX WPI; 2000-594183/56.

XX N-PSDB; AAA50500.

XX Novel recombinant lentivirus for inhibiting proliferation of smooth

XX muscle cells in e.g. restenosis, is replication deficient and comprises

XX a transgene encoding a cyclin dependent kinase inhibitor -

XX Example 1; Page 121; 126pp; English.

XX The present sequence is that of human p16, a cyclin dependent

XX kinase inhibitor (CDKi) that inhibits smooth muscle cell

XX proliferation. A claimed method for inhibiting smooth muscle cell

XX hyperproliferation involves transducing smooth muscle cells with a

XX replication-deficient recombinant adenovirus that lacks a functional

XX E1 region and a functional E4 region, and comprises a transgene

XX encoding a CDKi. The CDKi is selected from an INK4 family protein

XX such as human p16, a CIP/KIP family protein such as p27, active

CC fragments of these, or fusion proteins comprising (active fragments
CC of) an INK4 family protein and a CIP/KIP family protein (see AAY96046
CC cell hyperproliferation induced by injury caused by angioplasty,
CC stent placement or vein entrapment. It is useful for treating
CC vascular pathologies, e.g. restenosis. Also claimed are recombinant
CC lentiviruses encoding CDKis.
XX
SQ Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;
Best Local Similarity 98.7%; Pred. No. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSMFSDWLTAAARGVEVRALLEVALPNAPNSYGRRPDIQVMMGSAARVA 60
l:|||||
DB 1 mepaagssmepsadwltataaargrveevrallleagalpnapsygrripqymmggsarva 60
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120
|||||
61 ellllhgaepncadpatltrpvhdaaregfdltlvvlhragarlvdvdawgrlpvdlae 120
|||||
QY 121 LGHRDVARYLRAAAGTRGSHARIDAAEGPSDIPD 156
|||||
DB 121 lghrdvarylraaagtrgsharidaaegpsdipd 156
|||||

RESULT 12
AAY96067
ID AAY96067 standard; Protein; 156 AA.
XX
AC AAY96067;

XX 05-DEC-2000 (first entry)
XX Human cyclin dependent kinase inhibitor p16.
XX
XX Cyclin dependent kinase inhibitor; CDK1; INK4; human; p16;
KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;
KW endometriosis; psoriasis; vascular retinopathy; cytostatic;
KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;
KW antiproliferative; gene therapy.
XX
OS Homo sapiens.
XX
XX WO200052158-A1.

XX 08-SEP-2000.
XX
XX 28-FEB-2000; 2000WO-US04970.
XX
XX 01-MAR-1999; 99US-0122974.
PR 05-NOV-1999; 99US-0163682.
PR 09-DEC-1999; 99US-0457646.
XX
XX (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
XX Patel S, McArthur J, Gyuris J;
PI
XX WPI; 2000-565501/52.
DR N-PSDB; AAA50520.
XX

XX Inhibiting angiogenesis and treating angiogenesis-associated
PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial
PT cell with a recombinant virus having a transgene encoding a cyclin
PT dependent kinase inhibitor
XX
XX Example 1; Page 129; 138pp; English.
XX
XX The present sequence is that of human p16, a cyclin dependent
CC kinase inhibitor (CDK1) that inhibits angiogenesis. A claimed

CC method for inhibiting angiogenesis involves transducing an
CC epithelial cell with a transgene encoding (internalizable,
CC secretable) CDK1. The delivery system for the transgene may be a
CC liposome or a recombinant virus. The CDK1 is preferably a protein
CC of the CIP/KIP family such as p27, a protein of the INK4 family
CC such as p16, active fragments of these proteins, or a fusion of 2
CC CDK1 proteins such as p27 and p16 (see AAY96068-80). The method is
CC useful in treating conditions associated with angiogenesis, e.g.
CC neoplasia, rheumatoid arthritis, endometriosis, psoriasis and
CC vascular retinopathy (claimed). Alternatively, the transgene is
CC delivered to an auxiliary cell, and is expressed by that cell such
CC that the CDK1 is released into the blood and contacts the target
CC epithelial cell.
XX
SQ Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;
Best Local Similarity 98.7%; Pred. No. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSMFSDWLTAAARGVEVRALLEVALPNAPNSYGRRPDIQVMMGSAARVA 60
l:|||||
DB 1 mepaagssmepsadwltataaargrveevrallleagalpnapsygrripqymmggsarva 60
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120
|||||
61 ellllhgaepncadpatltrpvhdaaregfdltlvvlhragarlvdvdawgrlpvdlae 120
|||||
QY 121 LGHRDVARYLRAAAGTRGSHARIDAAEGPSDIPD 156
|||||
DB 121 lghrdvarylraaagtrgsharidaaegpsdipd 156
|||||

RESULT 13
AAY92921
ID AAY92921 standard; Protein; 156 AA.
XX
AC AAY92921;

XX 11-OCT-2000 (first entry)
XX Human multiple tumour suppressor 1 protein.
XX
XX Variant; human; multiple tumour suppressor; MTS; mutation; melanoma;
KW cancer; diagnosis.
XX
XX Homo sapiens.
XX
XX US6037462-A.
XX
XX 14-MAR-2000.
XX
XX 22-JUL-1998; 98US-0120130.
XX
XX 07-JUN-1995; 95US-0480810.
PR 18-MAR-1994; 94US-0214582.
PR 18-MAR-1994; 94US-0215086.
PR 18-MAR-1994; 94US-0215087.
PR 14-APR-1994; 94US-0227369.
PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;

XX WPI; 2000-269915/23.
XX N-PSDB; AAA11165.
XX
XX New mutants of the human multiple tumor suppressor gene, useful as
PT diagnostic markers of cancer, contain specific base alterations or
PT deletions

XX Disclosure; Column 61-62; 72pp; English.

PS The invention relates to variants (AA11196-A11206) of the human

XX multiple tumour suppressor 1 (MTS1) protein of which this sequence

CC represents the wild type sequence. The variants have the following

CC changes relative to the wild type coding sequence: A at any of positions

CC 265, 442, 330 and 329; T at any of positions 172, 238, 341 and 148 and

CC deletions of nucleotides 290-294, 172-179 or 128-129. The variants are

CC somatic mutations of MTS1, indicative of predisposition to melanoma and

CC many other cancers, so detecting them is useful for diagnosis, prognosis

CC and monitoring of cancer (including prenatal analysis). Cells and

CC animals that express the variants are useful as model systems for

CC identifying potential anticancer agents.

XX Sequence 156 AA;

SQ

Query Match 98.6%; Score 789; DB 21; Length 156;

Best Local Similarity 98.7%; Pred. No. 8.9e-85;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAAAGSMPEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGMSARVA 60

DB 1 mepaagssmepsadwlataaargveevrllleagalpnapnsygrripqvmmgmsarva 60

QY 61 ELLLLHGAEPNCADPATLTTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120

DB 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlhragardvdrdawgrlpvdlaee 120

QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

DB 121 lghrdvarylraaagtrgsharidaaegpsdipd 156

RESULT 14

AAV91102

ID AAV91102 standard; Protein; 156 AA.

XX

AC AAV91102;

XX

DT 12-SEP-2000 (first entry)

XX

DE Human multiple tumour suppressor MTS1 SEQ ID NO:2.

XX

KW Human; multiple tumour suppressor; MTS; somatic mutation; cancer;

KW diagnosis; germ line mutation; gene therapy; cytostatic; melanoma;

KW leukaemia; astrocytoma; glioblastoma; lymphoma; glioma;

KW Hodgkin's lymphoma.

OS Homo sapiens.

XX

PN US6060301-A.

XX

PD 09-MAY-2000.

XX

PF 14-JUL-1998; 98US-0115252.

XX

PR 07-JUN-1995; 95US-0480810.

PR 08-DEC-1997; 97US-0986147.

PR 18-MAR-1994; 94US-0214582.

PR 18-MAR-1994; 94US-0215086.

PR 18-MAR-1994; 94US-0215087.

PR 14-APR-1994; 94US-0227369.

PR 01-JUN-1994; 94US-0251938.

PR 17-MAR-1995; 95WO-US03316.

XX

PA (MYRI-) MYRIAD GENETICS INC.

XX

PI Kamb A;

XX

XX WPI; 2000-349676/30.

DR N-PSDB; AAA39353.

XX New vector useful for gene therapy of cancer associated with mutation

PT in tumor suppressor gene, comprises DNA sequence of multiple tumor

PT suppressor gene -

XX Disclosure; Column 63-64; 71pp; English.

XX The present invention describes a vector (I) comprising an isolated DNA

CC sequence of a multiple tumour suppressor (MTS) gene having a

CC polynucleotide sequence of the human MTS1E1-beta. (I) is useful for

CC introducing wild-type MTS function to a cancerous or pre-cancerous cell

CC which carries diminished or mutant MTS alleles for suppressing

CC neoplastic growth of the recipient cells. (I) is also useful for

CC increasing the level of expression of MTS gene even in tumour cells in

CC which the mutant gene is expressed at a normal level but the gene

CC product is not fully functional. A host cell transformed with (I) is

CC useful as a model system to study cancer remission and drug treatment

CC which promotes such remission. The present invention relates to somatic

CC mutations and germ line mutations in the MTS gene and their use in the

CC diagnosis and prognosis of human cancer e.g. melanoma, leukaemia,

CC astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, and

CC cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney,

CC stomach and rectum. The present sequence represents human MTS1, which is

CC used in the exemplification of the present invention.

XX Sequence 156 AA;

SQ

Query Match 98.6%; Score 789; DB 21; Length 156;

Best Local Similarity 98.7%; Pred. No. 8.9e-85;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAAAGSMPEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGMSARVA 60

DB 1 mepaagssmepsadwlataaargveevrllleagalpnapnsygrripqvmmgmsarva 60

QY 61 ELLLLHGAEPNCADPATLTTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120

DB 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlhragardvdrdawgrlpvdlaee 120

QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

DB 121 lghrdvarylraaagtrgsharidaaegpsdipd 156

RESULT 15

AAV59415

ID AAV59415 standard; Protein; 156 AA.

XX

AC AAV59415;

XX

DT 21-MAR-2000 (first entry)

XX

DE Human MTS1 protein sequence.

XX

KW MTS; human; polymorphism detection; cancer predisposition; astrocytoma;

KW Multiple Tumour Suppressor gene; melanoma; leukaemia; glioblastoma;

KW lymphoma; glioma; Hodgkin's lymphoma; chronic lymphocytic leukaemia;

KW therapy; MTS1.

OS Homo sapiens.

XX

PN US5989815-A.

XX

PD 23-NOV-1999.

XX

PF 29-APR-1997; 97US-0848251.

XX

PR 07-JUN-1995; 95US-0474083.

PR 18-MAR-1994; 94US-0214582.

PR 18-MAR-1994; 94US-0215086.

PR 18-MAR-1994; 94US-0215087.

PR 14-APR-1994; 94US-0227369.

Wed Oct 31 07:17:16 2001

us-09-016-869a-2.rag

PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03537.
XX
PA (UTAH) UNIV UTAH RES FOUND.
PA (MYRI-) MYRIAD GENETICS INC.
XX
XX
XX Skolnick MH, Cannon-Albright LA, Kamb A;
XX
XX WPI: 2000-070785/06.
DR N-PSDB; AAZ48770.
XX
XX Diagnosing a polymorphism associated with a predisposition for cancer -
XX
XX Claim 1; Column 61-64; 74pp; English.
XX
XX This sequence represents the human MTS1 protein.
CC The invention relates to a method for diagnosing a polymorphism
CC associated with a predisposition to cancer by detecting a germ-line
CC alteration of a wild-type Multiple Tumour Suppressor (MTS) gene or its
CC expression products in a human sample. The method comprises detecting a
CC germ-line alteration of a wild-type MTS gene or its expression products
CC in a human sample, the alteration indicating a predisposition to at least
CC one of the cancers. The cancer is selected from melanoma, leukaemia,
CC astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, breast,
CC chronic lymphocytic leukaemia (CLL), and cancers of the pancreas, breast,
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum. The method
CC may be used as the basis for developing very important diagnostic tests
CC capable of predicting the predisposition to cancer. The MTS gene is
CC involved in the progression of multiple tumour types and may provide
CC means for a general anti-cancer therapy by virtue of its ability to
CC suppress tumour growth.
XX
XX Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;
Best Local Similarity 98.7%; Pred. No. 8.9e-85;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db :|||||
Db 1 mepaagssmepsadwlataaargveevrallleagalpnapnsygrpiqvmmggsarva 60
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLHVRAGARLDVRDANGRLPVDLAE 120
Db :|||||
Db 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlhragarldvrdawgrlpvdlace 120
QY 121 Lghrdvarylraaaggtrgsnharidaaegpsdipd 156
Db :|||||
Db 121 lghrdvarylraaaggtrgsnharidaaegpsdipd 156

Search completed: October 31, 2001, 07:03:38
Job time: 65 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:02:33 ; Search time 54.92 Seconds
(without alignments)
58.487 Million cell updates/sec

Title: US-09-016-869A-2
Perfect score: 800
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAAGPSDIPD 156

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

1 number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2.6/prodata/1/1aa/5A-COMB.pep:*
2: /cgn2.6/prodata/1/1aa/5B-COMB.pep:*
3: /cgn2.6/prodata/1/1aa/6A-COMB.pep:*
4: /cgn2.6/prodata/1/1aa/6B-COMB.pep:*
5: /cgn2.6/prodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2.6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	800	100.0	156	2	US-08-627-610-2
2	800	100.0	156	2	US-08-306-511A-2
3	800	100.0	156	2	US-08-893-274-2
4	800	100.0	156	3	US-08-581-918A-2
5	800	100.0	156	4	US-08-346-147B-2
6	800	100.0	156	4	US-08-822-936-2
7	800	100.0	156	5	PCT-US95-04636-2
8	789.5	98.7	157	5	PCT-US96-05252-5
9	789	98.6	156	1	US-08-474-177-2
10	789	98.6	156	1	US-08-487-033-2
11	789	98.6	156	1	US-08-480-810-2
12	789	98.6	156	2	US-08-508-735-2
13	789	98.6	156	2	US-08-848-251-2
14	789	98.6	156	2	US-08-486-047-2
15	789	98.6	156	3	US-09-120-130-2
16	789	98.6	156	3	US-09-115-252-2
17	789	98.6	156	3	US-08-986-515-2
18	789	98.6	156	4	US-09-120-128-2
19	789	98.6	156	4	US-09-120-129-2
20	789	98.6	156	4	US-09-201-139-2
21	789	98.6	156	4	US-09-120-131-2
22	789	98.6	156	4	US-08-910-722-2
23	785	98.1	391	1	US-08-589-981-2
24	760	95.0	148	1	US-08-154-915-4
25	760	95.0	148	3	US-08-384-106A-16
26	760	95.0	148	3	US-08-384-106A-24
27	760	95.0	148	5	PCT-US93-09945-4

28	667.5	83.4	157	3	US-08-581-918A-12	Sequence 12, Appl
29	667.5	83.4	157	4	US-08-346-147B-12	Sequence 12, Appl
30	544	68.0	105	1	US-08-474-177-14	Sequence 14, Appl
31	544	68.0	105	1	US-08-487-033-14	Sequence 14, Appl
32	544	68.0	105	1	US-08-480-810-14	Sequence 14, Appl
33	544	68.0	105	2	US-08-508-735-14	Sequence 14, Appl
34	544	68.0	105	2	US-08-848-251-14	Sequence 14, Appl
35	544	68.0	105	2	US-08-486-047-14	Sequence 14, Appl
36	544	68.0	105	3	US-09-120-130-14	Sequence 14, Appl
37	544	68.0	105	3	US-09-115-252-14	Sequence 14, Appl
38	544	68.0	105	3	US-08-986-515-14	Sequence 14, Appl
39	544	68.0	105	4	US-09-120-128-14	Sequence 14, Appl
40	544	68.0	105	4	US-09-120-129-14	Sequence 14, Appl
41	544	68.0	105	4	US-09-201-139-14	Sequence 14, Appl
42	544	68.0	105	4	US-09-120-131-14	Sequence 14, Appl
43	533	66.6	130	2	US-08-627-610-8	Sequence 8, Appl
44	533	66.6	130	3	US-08-581-918A-8	Sequence 8, Appl
45	533	66.6	130	4	US-08-346-147B-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-627-610-2
; Sequence 2, Application US/08627610
; Patent No. 5919997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: Depinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; TITLE OF INVENTION: Regulation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-627-610-2

Query Match 100.0%; Score 800; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAFNSYGRRPQVMMGSRVA 60
Db 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAFNSYGRRPQVMMGSRVA 60

QY	61	ELLLLHGAEPNCADPATITRPVHDAAREGFGDTLVVLRHAGARLDVRDANGRLPVDLAE	120
Db	61	ELLLLHGAEPNCADPATITRPVHDAAREGFGDTLVVLRHAGARLDVRDANGRLPVDLAE	120
QY	121	LGHDRVARYLRAAAGTGRGSHARIDAAEGPSDIPD	156
Db	121	LGHDRVARYLRAAAGTGRGSHARIDAAEGPSDIPD	156

RESULT 2

US-08-306-511A-2

; Sequence 2, Application US/08306511A

; Patent No. 5962316

; GENERAL INFORMATION:

; APPLICANT: Beach, David H.

; APPLICANT: Demetrick, Douglas J.

; APPLICANT: Serrano, Manuel

; APPLICANT: Hannon, Gregory J.

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

; NUMBER OF INVENTION: Related Thereto

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/306,511A

; FILING DATE: 14-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: CSI-001CP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-306-511A-2

Query Match 100.0%; Score 800; DB 2; Length 156;

Best Local Similarity 100.0%; Pred. No. 1,6e-87;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY	1	MDPAAGSMPEPSADMLATAAARGVEEYRALLEAVALPNAPNSYGRRP IQVMMGSRVA	60
Db	1	MDPAAGSMPEPSADMLATAAARGVEEYRALLEAVALPNAPNSYGRRP IQVMMGSRVA	60
QY	61	ELLLLHGAEPNCADPATITRPVHDAAREGFGDTLVVLRHAGARLDVRDANGRLPVDLAE	120
Db	61	ELLLLHGAEPNCADPATITRPVHDAAREGFGDTLVVLRHAGARLDVRDANGRLPVDLAE	120
QY	121	LGHDRVARYLRAAAGTGRGSHARIDAAEGPSDIPD	156
Db	121	LGHDRVARYLRAAAGTGRGSHARIDAAEGPSDIPD	156

RESULT 3

US-08-893-274-2

; Sequence 2, Application US/08893274

Db 121 LGRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156

RESULT 4
US-08-581-918A-2
; Sequence 2, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordpad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,918A
; FILING DATE: 02-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/497,214
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-581-918A-2

Query Match 100.0%; Score 800; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEVRALLEAVALPNAPNSYGRRP1QVMMGSRVA 60

Db 1 MDPAGSSMEPSADWLATAAARGVEVRALLEAVALPNAPNSYGRRP1QVMMGSRVA 60
QY 61 ELLLLHCAPNCADPATLTTPVHDAAREGFDTLVVLHAGARLDYRDAGRLPVDLAE 120
Db 61 ELLLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLHAGARLDYRDAGRLPVDLAE 120
QY 121 LGRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
Db 121 LGRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156

RESULT 5
US-08-346-147B-2
; Sequence 2, Application US/08346147B
; Patent No. 6211334
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordpad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,147B
; FILING DATE: 29-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-346-147B-2

Query Match 100.0%; Score 800; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-87;

Matches	156;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	1	MPAAGSSWEFSADWLATAAARGVEEVRALLAEVALNPAENSYGRRPQVMMGMSARVA	60
Qy	61	ELLUHGAEPCADPATLTRPVHDAAREGFLDTLVYLHAGARLDVRDAMGRPLVDLAE	120
Db	61	ELLUHGAEPCADPATLTRPVHDAAREGFLDTLVYLHAGARLDVRDAMGRPLVDLAE	120
Qy	121	LGHROVARYLRAAAGGTRGNSNHARIDAAGPSDIPD	156
Db	121	LGHROVARYLRAAAGGTRGNSNHARIDAAGPSDIPD	156

RESULT 6
US-08-822-936--2
; Sequence 2, Application US/08822936
; Patent No. 6242575
; [REDACTED]
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated P27 Protein, Nucleic Acid
; TITLE OF INVENTION: Molecules Encoding Same, Methods of
; TITLE OF INVENTION: and Uses of Said Agents
; Identifying Agents Acting

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;
; NUMBER OF SEQUENCES: 10
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,936
; FILING DATE: 21-FEBRUARY-1997
;

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; ATTORNEY/AGENT INFORMATION:
;
; NAME: Vincent, Matthew P.
;
; REGISTRATION NUMBER: 36,709
;
; REFERENCE/DOCKET NUMBER: MIV-079.05
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (617) 832-1000
;
; TELEFAX: (617) 832-7000
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 156 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-822-936-2

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Query Match      100.0%; Score 800; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	MDPAAGSSWEPSADWLATAAARGVEEVRALLAEVALNPAPNSYGRRPDIQVMMGSRVA	60
Db	1	MDPAAGSSWEPSADWLATAAARGVEEVRALLAEVALNPAPNSYGRRPDIQVMMGSRVA	60
QY	61	ELLLLHGAEPNCADPATLTTPVHDDAAREGFDTLVVYLHRAGARLDVDRDAGRLPVDLAAE	120
Db	61	ELLLLHGAEPNCADPATLTTPVHDDAAREGFDTLVVYLHRAGARLDVDRDAGRLPVDLAAE	120
QY	121	LGHRDVARYLRAAAGGTRGNSNHARIDAAEGSPDIP	156

121 LGHRDVARYLRAAGTRGCSNHARIDA AEGPSDIPD 156
Db

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RESULT      7
PCT-US95-04636-2
; Sequence 2, Application PC/TUS9504636
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04636-2

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Query Match	100.0%;	Score 800;	DB 5;	Length 156;
Best Local Similarity	100.0%;	Pred. No. 1.6e-87;		
Matches 156;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Db	60	1	MDPAAGSSWEPSADWLATAAARGVEVRRALLLEAVALNPAPNSYGRRTQVMMGMSARVA	60
Qy	120	61	ELLHLGHAEPNCADPATLTRVHDAAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE	120
Db	120	61	ELLHLGHAEPNCADPATLTRVHDAAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE	120
Qy	156	121	LGHKDVARYLRAAAGGTGSGNHARIDAAEGSPDIPD	156
Db	156	121	LGHKDVARYLRAAAGGTGSGNHARIDAAEGSPDIPD	156

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RESULT      8
PCT-US96-05252-5
; Sequence 5, Application PC/TUS9605252
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION:  pl9: A Cell Cycle Inhibitor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Townsend and Townsend and Crew
; STREET:  One Market Plaza, Steuart Street Tower
; CITY:  San Francisco
; STATE:  California
; COUNTRY:  USA
; ZIP:  94105-1492
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05252
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 02307B-059910PC
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..157
OTHER INFORMATION: /note= "human p16"
PCT-US96-05252-5

Query Match 98.7%; Score 789.5; DB 5; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.9e-86;
Matches 156; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVA 60
Db 1 MDPAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVA 60
QY 61 E-LLLLHGAEPNCADPATITRPVHDAAREGFLDTLVLLHRAAGRLDVRDAGRLPVDLAE 119
Db 61 ELLLLHGAEPNCADPATITRPVHDAAREGFLDTLVLLHRAAGRLDVRDAGRLPVDLAE 120
QY 120 ELGHRDVARYLRAAAGTRGSHARIDAAEGPSDIPD 156
Db 121 ELGHRDVARYLRAAAGTRGSHARIDAAEGPSDIPD 157

US-08-474-177-2
Sequence 2, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-177-2

Query Match 98.6%; Score 789; DB 1; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVA 60
Db 1 MDPAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVA 60
QY 61 ELLLLHGAEPNCADPATITRPVHDAAREGFLDTLVLLHRAAGRLDVRDAGRLPVDLAE 120
Db 61 ELLLLHGAEPNCADPATITRPVHDAAREGFLDTLVLLHRAAGRLDVRDAGRLPVDLAE 120
QY 121 LGHRDVARYLRAAAGTRGSHARIDAAEGPSDIPD 156
Db 121 LGHRDVARYLRAAAGTRGSHARIDAAEGPSDIPD 156

RESULT 10
US-08-487-033-2
Sequence 2, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1E1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/487,033
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/03316
;; FILING DATE: 17-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/251,938
;; FILING DATE: 01-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,087
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,086
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/227,369
;; FILING DATE: 14-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/214,582
;; FILING DATE: 18-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109348-C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-962-4810
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 156 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-487-033-2

Query Match 98.6%; Score 789; DB 1; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAPNSYGRRPQVMMGSAARVA 60
Db 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAPNSYGRRPQVMMGSAARVA 60
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAE 120
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAE 120
QY 121 LGRDVARVLRRAAGGTRGSHARIDAEGPSDIPD 156
Db 121 LGRDVARVLRRAAGGTRGSHARIDAEGPSDIPD 156

RESULT 11
US-08-480-810-2
; Sequence 2, Application US/08480810
; Patent No. 5801236
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/480,810
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/03316
;; FILING DATE: 17-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/251,938
;; FILING DATE: 01-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,087
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,086
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/227,369
;; FILING DATE: 14-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/214,582
;; FILING DATE: 18-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109348
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-962-4810
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 156 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-480-810-2

Query Match 98.6%; Score 789; DB 1; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAPNSYGRRPQVMMGSAARVA 60
Db 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAPNSYGRRPQVMMGSAARVA 60
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAE 120
Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAE 120
QY 121 LGRDVARVLRRAAGGTRGSHARIDAEGPSDIPD 156
Db 121 LGRDVARVLRRAAGGTRGSHARIDAEGPSDIPD 156

RESULT 12
US-08-508-735-2
; Sequence 2, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508/735
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-508-735-2

Query Match          98.6%; Score 789; DB 2; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPAGSSMEPSADWLATAAARGVEEVRAALLEAVALEPNAPNSYGRRPPIQVMMMGSAVA 60
Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRAALLEAGALPNAPNSYGRRPPIQVMMMGSAVA 60

Qy 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDIAEE 120
Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDIAEE 120

Qy 121 LGRDVARYLRAAAGGTGRGSHARIDAAREGSDIPD 156
Db 121 LGRDVARYLRAAAGGTGRGSHARIDAAREGSDIPD 156

LT 13
US-08-848-251-2
; Sequence 2, Application US/08848251
; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,251
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/474,083
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-848-251-2

Query Match          98.6%; Score 789; DB 2; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPAGSSMEPSADWLATAAARGVEEVRAALLEAVALEPNAPNSYGRRPPIQVMMMGSAVA 60
Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRAALLEAGALPNAPNSYGRRPPIQVMMMGSAVA 60

Qy 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDIAEE 120
Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDIAEE 120

Qy 121 LGRDVARYLRAAAGGTGRGSHARIDAAREGSDIPD 156
Db 121 LGRDVARYLRAAAGGTGRGSHARIDAAREGSDIPD 156

RESULT 14
US-08-486-047-2
; Sequence 2, Application US/08486047
; Patent No. 5994095
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-047-2

Query Match 98.6%; Score 789; DB 2; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADMLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGSRVA 60
:|||||
1 MEPAAGSSMEPSADMLATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGSRVA 60
|||||

QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
|||||
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
|||||

Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
|||||

QY 121 LGRDVARVLRAGAGTGRGSHARIDAAEGPSDIPD 156
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121 LGRDVARVLRAGAGTGRGSHARIDAAEGPSDIPD 156
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Db 121 LGRDVARVLRAGAGTGRGSHARIDAAEGPSDIPD 156
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RESULT 15
US-09-120-130-2
; Sequence 2, Application US/09120130
; Patent No. 6037462
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
```

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; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,130
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,810
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-120-130-2

Query Match 98.6%; Score 789; DB 3; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADMLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGSRVA 60
:|||||
1 MEPAAGSSMEPSADMLATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGSRVA 60
|||||

Db 1 MEPAAGSSMEPSADMLATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGSRVA 60
|||||

QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
|||||
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
|||||

Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
|||||

QY 121 LGRDVARVLRAGAGTGRGSHARIDAAEGPSDIPD 156
|||||
121 LGRDVARVLRAGAGTGRGSHARIDAAEGPSDIPD 156
|||||

Db 121 LGRDVARVLRAGAGTGRGSHARIDAAEGPSDIPD 156
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Search completed: October 31, 2001, 07:04:45
Job time: 132 sec